

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2003, 22:31:05 ; Search time 3253 Seconds
(without alignments)
286.286 Million cell updates/sec

Title: US-09-895-435-3

Perfect score: 32

Sequence: 1 taatacaacaataattattgtgttatta 32

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hg.*

3: gb_in.*

4: gb_ov.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_ph.*

9: gb_pl.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_mu.*

21: em_or.*

22: em_ov.*

23: em_ph.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_inv.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rtd.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	32	100.0	4149	1	BTTN4430	X07651 Bacillus th
2	32	100.0	9672	1	BTPG12XX	X13481 Bacillus th
C 3	25.6	80.0	4149	1	BTTN4430	X07651 Bacillus th
C 4	25.6	80.0	9672	1	BTPG12XX	X13481 Bacillus th
C 5	24.6	76.9	164303	2	AC027541	AC027541 Homo sapi
6	24.6	76.9	176759	2	AC100807	AC100807 Homo sapi
7	23	71.9	81885	10	AL663040	AL663040 Mouse DNA
C 8	23	71.9	94535	9	AC083886	AC083886 Homo sapi
9	23	71.9	115359	8	AC003028	AC003028 Arabidops
C 10	23	71.9	119819	9	AL161631	AL161631 Human DNA
C 11	23	71.9	123579	2	AC017792	AC017792 Drosophi
C 12	23	71.9	145734	2	AC011096	AC011096 Homo sapi
C 13	23	71.9	151535	2	AC084188	AC084188 Homo sapi
C 14	23	71.9	164982	3	AC008254	AC008254 Drosophi
C 15	23	71.9	176036	3	AC009258	AC009258 Drosophi
C 16	23	71.9	194905	9	AC068896	AC068896 Homo sapi
C 17	22.6	70.6	102507	9	HSJ324N14	HSJ324N14 Human DNA
C 18	22.6	70.6	157564	2	AC025996	AC025996 Homo sapi
C 19	22.6	70.6	170073	2	AL845419	AL845419 Danio rer
C 20	22.6	70.6	171179	2	AC034140	AC034140 Homo sapi
C 21	22.6	70.6	182740	2	AC121330	AC121330 Homo sapi
C 22	22.6	70.6	198742	2	AL355360	AL355360 Homo sapi
C 23	22.4	70.0	363	8	MISCARS	X00436 Yeast mtDNA
24	22.4	70.0	676	8	YSCMTAP92	J01461 Yeast (S.ce
25	22.4	70.0	909	8	MISC28	X00818 Yeast mitoc
26	22.4	70.0	3542	8	YSCMTG16	L36900 Saccharomyc
27	22.4	70.0	33507	7	AY082070	AY082070 Bacteriop
28	22.4	70.0	85779	8	SCE011856	AY011856 Saccharom
29	22.4	70.0	91061	2	AC087139	AC087139 Mus muscu
C 30	22.4	70.0	132000	2	AC116976	AC116976 Dictyoste
31	22.4	70.0	165509	2	AC009886	AC009886 Homo sapi
C 32	22.4	70.0	168614	9	AL357672	AL357672 Human DNA
C 33	22.4	70.0	170672	2	AC113127	AC113127 Mus muscu
34	22.4	70.0	176968	2	AC129250	AC129250 Rattus no
C 35	22.4	70.0	179779	2	AC113106	AC113106 Mus muscu
C 36	22.4	70.0	180279	2	AC109717	AC109717 Rattus no
37	22.4	70.0	181835	9	AC026124	AC026124 Homo sapi
C 38	22.4	70.0	186681	9	AC068643	AC068643 Homo sapi
C 39	22.4	70.0	199806	2	AC025580	AC025580 Homo sapi
C 40	22.4	70.0	202490	2	AC121884	AC121884 Mus muscu
C 41	22.4	70.0	271144	9	HSXDPB	AL590763 Homo sapi
C 42	22.2	69.4	195761	2	AC113204	AC113204 Mus muscu
C 43	22	68.8	87767	2	AC014497	AC014497 Drosophi
44	22	68.8	94588	2	AC116196	AC116196 Rattus no
45	22	68.8	150587	3	AC007549	AC007549 Drosophi

ALIGNMENTS

RESULT 1
BTTN4430
LOCUS
DEFINITION
ACCESSION
X07651
VERSION
X07651.1
KEYWORDS
SOURCE
ORGANISM
Bacillus thuringiensis
REFERENCE
AUTHORS
TITLE

4149 bp DNA linear BCT 12-SEP-1993
Bacillus thuringiensis transposon Tn4430.
X07651
GI:40347
plasmid; resolvase; tnpA gene; tnpI gene; transposase; transposon.
Bacillus thuringiensis.
Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
1. (bases 1 to 4149)
Mahillon, J. and Lereclus, D.
Structural and functional analysis of Tn4430: identification of an
integrase-like protein involved in the co-integrate-resolution

Pred. No. is the number of results predicted by chance to have a

process
EMBO J. 7 (5), 1515-1526 (1988)
JOURNAL
MEDLINE 88312602
PUBMED 2842151
COMMENT
Data kindly reviewed (03-APR-1989) by Lereclus D.
FEATURES
source
Location/Qualifiers
1..4149
/organism="Bacillus thuringiensis"
/strain="HI.1"
/db_xref="taxon:1428"
/map="plasmid pG12"
/clone_lib="pG120"
/clone_lib="pBR322"
1..38
/note="inverted repeat A"
247..1101
/note="put. resolvase Tnp I (AA 1 - 284)"
/codon_start=1
/transl_table=11
/protein_id="CAA30491.1"
/db_xref="GI:40348"
/db_xref="SWISS-PROT:P10020"
/translation="MDVAKQFSSYLKQENKTENTVQGYTSGIRQYIKWPEGSDYDKRLT
KLYRQNIIEVLSYLVNKLNAKSNHKKISLAKFNEFLIQKSGQDQVILKIDMLKQ
QTVYASPTQIVLQVKKFLQSVLEDDNNKRNATATLLAYTVGRISALSIKMDFNLO
TGECHIRSGKQKQRIVLLSKVLSAIDKLYIDRKTSTAHESPYLFISSKREKLDRT
VWNRIFKSYSNVITPHQLRHFFCTNAIEKGFSEIHEVANQAGHSNIHTLLTYNPNLOQ
LKNKMWELL"
1120..4083
/note="transposase Tnp A (AA 1 - 987)"
/codon_start=1
/transl_table=11
/protein_id="CAA30492.1"
/db_xref="GI:40349"
/db_xref="SWISS-PROT:P10021"
/translation="MGVKQLSEAGORNELMDLSRLTEWDLVTRFTSKDHLHLILKHR
RGYNRLGAFRLVLRIPGWSLTKEDIPQYVAYVTSRLRIPPEELVYAKRGNTLW
EHGEIRTEYGVQNFSEYKTELLQFLVQQAMDNNTLYLIEITISLRKTKVLLPAM
YVIEDVWEAKQADQKVYSILHDLGVQEQDQDALLPTINGKSPFLAWLKDVPAQ
SPESFLKVIDRLOFVKQIGLITDTTKINTNRLQRLARLGSKEPYAFRRFNEVKRYSM
LVSFLEITQDLIDYAEIHDRLMNLTQKKEQDEIQQANGKLNKELIQFTVCG
TLFEAKETGKDAFALDEVMSWNEVESVEAKOLSRPLNDYDOLLNTRYSVYRYA
PTLLRSHPRAKSCPEVLOAQDTHELVNTEGKRVKPHGAPLHFSVNRWQKHVVDDG
NINRHYELAAITELNRHRSRDIIVSGSRHKKAFDDYLIPIYDEMNEVSNIPAGSKLL
LKAEDYITDRINKLHLEWLSKNSKELEGVDISQGLHVERLDRGTPEAKAFSKLL
HSMPLRIKTLDLIEVASWTGFHDQFIHASTNQSPDQEQNIIVLATLMAGTNIIGLTK
MAEATPGISYROMANASOMRYDDAMVRAQSILVNFQEQKSLGWDGDTSSDGMH
LSTAVSLHADSHPHYTGKGGTIVRFVSDQLSAYHKVITTNARDAHLVDGLLHHE
TDLKIPEHTYDQVDFATLHLLGFRAPIRDLATKLFSPGGEYENYQALL
TGKINKVLKENYEDIRRLAYSVOGTQVSSALIMGKLSYARONKLATALGEMGRLEK
TLFTLDYISNKAVRRVQGLNKGAINALARTIFFGQGFERRALQDOLQASALN
IIINAIASVNTVYMERKAVEELKARGEFFREDLPMYAPLWGLWGHIIHFLGEYFEGHLHDIG
QMLRPLRIKPEPYS"
4112..4149
/note="inverted repeat A'"
repeat_unit 1506 a 685 c 776 g 1182 t
BASE COUNT
ORIGIN
Query Match 100.0%; Score 32; DB 1; Length 4149;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TAATACACACAATTAATTTGTTGTGTTATTA 32
|||||
DB 113 TAATACACACAATTAATTTGTTGTGTTATTA 144
|||||
RESULT 2
BTG12XX
LOCUS Bacillus thuringiensis plasmid pG12 with transposon Tn430.
DEFINITION
ACCESSION X13481


```

RESULT 5
AC027541/c
LOCUS
DEFINITION
  Homo sapiens chromosome 8 clone RP11-324F11 map 8, linear HTG 17-AUG-2002
  IN PROGRESS ***, 1 ordered piece.
AC027541.11 GI:22296720
VERSION
  HTG: HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
KEYWORDS
  human.
SOURCE
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 164303)
  Birren,B., Nussbaum,C. and Lander,E.
  Homo sapiens chromosome 8, clone RP11-324F11
  Unpublished
  2 (bases 1 to 164303)
  Birren,B., Linton,L., Nussbaum,C., Lander,E., Abraham,H., Allen,N.,
  Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
  Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
  Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
  Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
  Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
  Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
  Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
  Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
  Klein,J., LaRoque,K., Lamazares,R., Landers,T., Lehoczy,J.,
  Levine,R., Liu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
  McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
  Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J.,
  Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
  Pisan,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
  Roy,A., Santos,R., Schauer,S., Severi,P., Spencer,B.,
  Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
  Tesfaye,S., Theodores,J., Tirrell,A., Travers,M., Trigilio,J.,
  Vassiliev,H., Viel,R., Vo,A., Willson,B., Wu,X., Wyman,D., Ye,W.J.,
  Young,G., Zainoun,J., Zimmer,A. and Zody,M.
  Direct Submission
  Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
  Research, 320 Charles Street, Cambridge, MA 02141, USA
  3 (bases 1 to 164303)
  Birren,B., Nussbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
  Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,
  Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
  Cooke,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
  Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
  Gardyna,S., Gord,S., Graham,L., Grand-pierre,N., Hagos,B.,
  Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
  Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-roh,K.,
  Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
  McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mienga,V.,
  Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
  O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
  Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
  Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severi,P.,
  Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
  Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
  Viel,R., Vo,A., Willson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
  Zembek,L., Zimmer,A. and Zody,M.
  Direct Submission
  Submitted (17-AUG-2002) Whitehead Institute/MIT Center for Genome
  Research, 320 Charles Street, Cambridge, MA 02141, USA
  On Aug 17, 2002 this sequence version replaced gi:22123707.
  All repeats were identified using RepeatMasker:
  Smit, A.F.A. & Green, P. (1996-1997)
  http://ftp.genome.washington.edu/RM/RepeatMasker.html
  ----- Genome Center
  Center: Whitehead Institute/ MIT Center for Genome Research
  Web site: http://www-seq.wi.mit.edu
  Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information
Center project name: L8782
Center clone name: 324_F_11
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 164303: contig of 164303 bp in length.
FEATURES
  source
    Location/Qualifiers
      1..164303
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /chromosome="8"
      /map="8"
      /clone="RP11-324F11"
      /clone_lib="RPCI-11 Human Male BAC"
  BASE COUNT 48256 a 33368 c 34914 g 47765 t
  ORIGIN
    Query Match 76.9%; Score 24.6; DB 2: Length 164303;
    Best Local Similarity 87.1%; Pred. No. 44;
    Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
    QY 2 AATACACACATATTAAATTTGTTGTTATTA 32
    1111111111111111111111111111111111
    Db 116845 AATACATACATATTAAATTTGTTGTTATTA 116815
    1111111111111111111111111111111111
    RESULT 6
    AC100807
    LOCUS
    DEFINITION
      Homo sapiens chromosome 8 clone CTD-2534J5 map 8, linear HTG 20-AUG-2002
    PROGRESS ***, 2 unordered pieces.
    AC100807
    AC100807.2 GI:22325314
    HTG: HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
    SOURCE
      ORGANISM
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      1 (bases 1 to 176759)
      Birren,B., Nussbaum,C. and Lander,E.
      Homo sapiens chromosome 8, clone CTD-2534J5
      Unpublished
      2 (bases 1 to 176759)
      Birren,B., Linton,L., Nussbaum,C., Lander,E., Ali,A., Allen,N.,
      Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
      Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
      Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,A.,
      Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
      Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
      Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
      Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
      Jones,C., Kamat,A., Karatas,A., Kells,C., LaRoque,K.,
      Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
      MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
      McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
      Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C.,
      Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
      Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rise,C., Rogov,P.,
      Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severi,P.,
      Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
      Tesfaye,S., Theodore,J., Topham,K., Travers,M., Trigilio,J.,
      Viel,R., Vo,A., Willson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
      Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  REFERENCE
    AUTHORS
      Birren,B., Nussbaum,C. and Lander,E.
    JOURNAL
      Unpublished
    REFERENCE
      1 (bases 1 to 176759)
      Birren,B., Linton,L., Nussbaum,C., Lander,E., Ali,A., Allen,N.,
      Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
      Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
      Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,A.,
      Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
      Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
      Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
      Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
      Jones,C., Kamat,A., Karatas,A., Kells,C., LaRoque,K.,
      Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
      MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
      McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
      Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C.,
      Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
      Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rise,C., Rogov,P.,
      Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severi,P.,
      Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
      Tesfaye,S., Theodore,J., Topham,K., Travers,M., Trigilio,J.,
      Viel,R., Vo,A., Willson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
      Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  REFERENCE
    AUTHORS
      Birren,B., Nussbaum,C. and Lander,E.
    JOURNAL
      Unpublished
    REFERENCE
      2 (bases 1 to 176759)
      Birren,B., Linton,L., Nussbaum,C., Lander,E., Ali,A., Allen,N.,
      Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
      Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
      Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,A.,
      Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
      Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
      Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
      Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
      Jones,C., Kamat,A., Karatas,A., Kells,C., LaRoque,K.,
      Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
      MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
      McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
      Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C.,
      Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
      Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rise,C., Rogov,P.,
      Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severi,P.,
      Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
      Tesfaye,S., Theodore,J., Topham,K., Travers,M., Trigilio,J.,
      Viel,R., Vo,A., Willson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
      Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

```

	AL663040	8185 bp	DNA	linear	ROD 16-FEB-2002
	LOCUS				
	DEFINITION	Mouse DNA sequence from clone RP23-6LM22 on chromosome 11, complete			

REFERENCE
AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 94535)
 Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Albrooks, S.L., Amarantunga, H.C., Are, J.R., Ayale, M., Banks, T., Barbaria, J., Benton, J., Blinage, K., Blankenbush, K., Bonnin, D., Bouck, J., Bowie, S., Brile, M., Brown, E., Brown, M., Bryant, N.P., Buhay, P., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Garroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Haley, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., He, X., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lied, C., Liu, J., Liu, W., Lousaged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mathiney, E., McLeod, M.P., Meador, M., Mel, G., Metzger, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Moore, S., Morgan, M., Moorish, T., Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenwo, S., Ogih, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.D., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoostari, N., Sisson, I., Sodergren, E., Sonaite, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Worley, K., Wu, C., Wu, Y., Williamson, A., Wleczky, R., Woodson, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Naylor, S.L., Weinstock, G. and Gibbs, R.

Direct Submission
 Unpublished
 2 (bases 1 to 94535)
 Worley, K.C.
 Direct Submission
 Submitted (05-OCT-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 94535)
 Worley, K.C.
 Direct Submission
 Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 4 (bases 1 to 94535)
 Worley, K.C.
 Direct Submission
 Submitted (26-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 On Jul 26, 2002 this sequence version replaced gi:21952622.
 INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTSs, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annot>

FEATURES

Location/Qualifiers

1. .94535
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="3"
 /clone="RP11-364F11"
 1145..1277

repeat_region

/rpt_family="MIR"
 1365..1393

repeat_region

/rpt_family="AT-rich"
 complement(3179..3270)

repeat_region

/rpt_family="L2"
 4425..4494

repeat_region

/rpt_family="(TC)n"
 5662..5848

repeat_region

/rpt_family="MIR"
 5911..6195

repeat_region

/rpt_family="AluSc"
 complement(6661..6806)

repeat_region

/rpt_family="LTR33"
 complement(6904..7076)

repeat_region

/rpt_family="LTR33"
 7269..7372

repeat_region

/rpt_family="L2"
 complement(9820..9931)

repeat_region

/rpt_family="L1MA8"
 9932..10236

repeat_region

/rpt_family="AluSc"
 complement(10237..10651)

repeat_region

/rpt_family="L1MA8"
 11144..11681

repeat_region

/rpt_family="L2"
 complement(12092..12167)

repeat_region

/rpt_family="MIR"
 12470..12754

repeat_region

/rpt_family="L1MA1"
 complement(14119..14672)

repeat_region

/rpt_family="MIR"
 complement(14920..15017)

repeat_region

/rpt_family="MER5A"
 15660..15729

repeat_region

/rpt_family="MIR"
 16326..16354

repeat_region

/rpt_family="(CA)n"
 complement(16742..16969)

repeat_region

/rpt_family="MIR"

[illegible]

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at

http://www.sanger.ac.uk/HGP/Chr9
RP11-70K10 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see

http://www.chori.org/dacpac/home.htm
VECTOR: pBACe3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-70K10 It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true left end of clone RP11-35N6 is at 117820 in this sequence. The true right end of clone RP11-80H12 is at 2000 in this sequence.

Location/Qualifiers
1. .119819

/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/clone="RP11-70K10"
/clone_lib="RPCI-11.1"

BASE COUNT 36242 a 22548 c 23464 g 37565 t

ORIGIN

Query Match 71.9%; Score 23; DB 9; Length 119819;
Best Local Similarity 83.9%; Pred. No. 1.6e+02;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 TAATACACACAAATTAATTGTTGTTGTTATT 31
||||| ||||||| ||||| ||||| |||||

DB 71981 TAATAAACACAAATATTCATTTTATTATATT 71951

RESULT 11

AC017792/c

LOCUS

DEFINITION

AC017792 123579 bp DNA linear HTG 09-DEC-1999

Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered pieces.

AC017792

AC017792.1 GI:6553398

HTG: HTGS_PHASE2

Drosophila melanogaster.

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 123579)

Adams, M. and Venter, J.C.

Direct Submission

Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA

This sequence was identified as CDM:10212105 by the submitter. For more information on this record e-mail to fly@celera.com.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers

1. .123579

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

BASE COUNT 35860 a 25889 c 26036 g 35734 t

ORIGIN

Query Match 71.9%; Score 23; DB 2; Length 123579;
Best Local Similarity 83.9%; Pred. No. 1.6e+02;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 AATACACACAAATTAATTGTTGTTGTTATT 32
||||| ||||||| ||||||| |||||

DB 36974 AACAAACACATATTAATTGTTGTTATT 36944

RESULT 12

AC011096/c

LOCUS

DEFINITION

AC011096 145734 bp DNA linear HTG 28-SEP-2000

Homo sapiens clone RP11-2D21, WORKING DRAFT SEQUENCE, 4 unordered pieces.

AC011096

AC011096.3 GI:10334908

HTG: HTGS_PHASE1; HTGS_DRAFT.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

1 (bases 1 to 145734)

Homo sapiens, clone RP11-2D21

Unpublished

2 (bases 1 to 145734)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Bouckhalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArelano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hags, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczy, J., Lien, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

Direct Submission

Submitted (01-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Sep 28, 2000 this sequence version replaced gi:7717103.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L1511

Center clone name: 2.D-21

----- Summary Statistics

Sequencing vector: M13; M7815; 93% of reads

Chemistry: Dye-terminator Big Dye; 97% of reads

Chemistry: Dye-terminator Big Dye; 97% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 144340 bases at least Q40

Consensus quality: 145024 bases at least Q30

Consensus quality: 145305 bases at least Q20

Insert size: 150000; agarose-1p

Insert size: 145434; sum-of-contigs

Quality coverage: 7.7 in Q20 bases; a.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

```

* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
*
* 1 41082: contig of 41082 bp in length
* 41083 41182: gap of 100 bp
* 41183 55282: contig of 14100 bp in length
* 55283 55382: gap of 100 bp
* 55383 111365: contig of 55983 bp in length
* 111366 111468: gap of 100 bp
* 111466 145734: contig of 34269 bp in length.
FEATURES
    Location/Qualifiers
        1..145734
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="RP11-2D21"
            /clone_lib="RPC1-11 Human Male BAC"
        1..41082
            /note="assembly_fragment"
            clone_end:SP6
            vector_side:left
        41183..55282
            /note="assembly_fragment"
        55383..111365
            /note="assembly_fragment"
        111466..145734
            /note="assembly_fragment"
            clone_end:T7
            vector_side:right"
BASE COUNT 44971 a 27856 c 27629 g 44978 t 300 others
ORIGIN
Query Match 71.9%; Score 23; DB 2: Length 145734;
Best Local Similarity 83.9%; Pred No. 1.5e+02;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 TAATACACACAATATTATTCGTGTGTTATT 31
||||| ||||||||| ||| ||| |||
Db 59434 TAATAAACACAATATTCATTTTATTATATT 59404

RESULT 13
AC084188 151535 bp DNA linear HTG 15-JAN-2001
LOCUS Homo sapiens clone RP11-240G10, WORKING DRAFT SEQUENCE, 27
DEFINITION
Homo sapiens clone RP11-240G10, WORKING DRAFT SEQUENCE, 27
unordered pieces.
AC084188
AC084188.2 GI:12229375
VERSION
HTG: HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS
Homo sapiens
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 151535)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-240G10
Unpublished
2 (bases 1 to 151535)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bada,F., Boguslavsky,L.,
Boukhalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
Choepei,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,
Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L.,
Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G.,
Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McKernan,K.,
McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,
O'Donnelli,P., O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Rieback,M., Riley,R.,
Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,

```

```

Sougnuez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrelli,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (14-OCT-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jan 15, 2001 this sequence version replaced gi:10801416.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L11461
Center clone name: 240_G_10
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 142103 bases at least Q40
Consensus quality: 146385 bases at least Q30
Consensus quality: 148123 bases at least Q20
Insert size: 157000; agarose-fp
Quality coverage: 148935; sum-of-contigs
Quality coverage: 4.2 in Q20 bases; agarose-fp
Quality coverage: 4.4 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 27 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 241: contig of 241 bp in length
* 242 341: gap of 100 bp
* 342 1664: contig of 1323 bp in length
* 1665 1764: gap of 100 bp
* 1765 3932: contig of 2168 bp in length
* 3933 4032: gap of 100 bp
* 4033 5773: contig of 1741 bp in length
* 5774 5873: gap of 100 bp
* 5874 7178: contig of 1305 bp in length
* 7179 7278: gap of 100 bp
* 7279 8531: contig of 1253 bp in length
* 8532 8631: gap of 100 bp
* 8632 10607: contig of 1976 bp in length
* 10608 10707: gap of 100 bp
* 10708 33534: contig of 22827 bp in length
* 33535 33634: gap of 100 bp
* 33635 35523: contig of 1889 bp in length
* 35524 35623: gap of 100 bp
* 35624 38893: contig of 3270 bp in length
* 38894 38993: gap of 100 bp
* 38994 41672: contig of 2679 bp in length
* 41673 41772: gap of 100 bp
* 41773 44425: contig of 2653 bp in length
* 44426 44525: gap of 100 bp
* 44526 47448: contig of 2923 bp in length
* 47449 47548: gap of 100 bp
* 47549 52374: contig of 4726 bp in length
* 52375 52775: gap of 100 bp
* 52775 55715: contig of 3341 bp in length
* 55716 55815: gap of 100 bp
* 55816 58645: contig of 2830 bp in length
* 58646 58745: gap of 100 bp
* 58746 61720: contig of 2975 bp in length

```

TITLE
JOURNAL
COMMENT

```

* 61721 61820: gap of 100 bp
* 61821 66287: contig of 4467 bp in length
* 66288 66387: gap of 100 bp
* 66388 71117: contig of 4730 bp in length
* 71118 71217: gap of 100 bp
* 71218 77151: contig of 5934 bp in length
* 77152 77251: gap of 100 bp
* 77252 87532: contig of 10281 bp in length
* 87533 87632: gap of 100 bp
* 87633 94594: contig of 6962 bp in length
* 94595 94694: gap of 100 bp
* 94695 103008: contig of 8314 bp in length
* 103009 103108: gap of 100 bp
* 103109 113634: contig of 10526 bp in length
* 113635 113734: gap of 100 bp
* 113735 128598: contig of 14864 bp in length
* 128599 128698: gap of 100 bp
* 128699 149705: contig of 21007 bp in length
* 149706 149805: gap of 100 bp
* 149806 151535: contig of 1730 bp in length.

```

FEATURES

source

```

1. .151535
   /organism="Homo sapiens"
   /db_xref="taxon:9606"
   /clone="RP11-240G10"
   /clone_lib="RPC1-11 Human Male BAC"

```

misc_feature

```

1. 241
   /note="assembly_fragment"
   clone_end:SP6
   vector_side:left
   342. .1664

```

misc_feature

```

/note="assembly_fragment"

```

misc_feature

```

1765. 3932
/note="assembly_fragment"

```

misc_feature

```

4033. .5773
/note="assembly_fragment"

```

misc_feature

```

5874. 71178
/note="assembly_fragment"

```

misc_feature

```

7279. 8531
/note="assembly_fragment"

```

misc_feature

```

8632. 10607
/note="assembly_fragment"

```

misc_feature

```

10708. .33534
/note="assembly_fragment"

```

misc_feature

```

33635. .35523
/note="assembly_fragment"

```

misc_feature

```

35624. 38893
/note="assembly_fragment"

```

misc_feature

```

38994. .41672
/note="assembly_fragment"

```

misc_feature

```

41773. .44425
/note="assembly_fragment"

```

misc_feature

```

44526. 47448
/note="assembly_fragment"

```

misc_feature

```

47549. .52274
/note="assembly_fragment"

```

misc_feature

```

52375. .55715
/note="assembly_fragment"

```

misc_feature

```

55816. 58645
/note="assembly_fragment"

```

misc_feature

```

58746. .61720
/note="assembly_fragment"

```

misc_feature

```

61821. .66287
/note="assembly_fragment"

```

misc_feature

```

66388. 71117
/note="assembly_fragment"

```

misc_feature

```

71218. .77151
/note="assembly_fragment"

```

misc_feature

```

77252. .87532
/note="assembly_fragment"

```

misc_feature

```

87633. 94594
/note="assembly_fragment"

```

misc_feature

```

94695. .103008

```

```

/note="assembly_fragment"
103109. .113634
/note="assembly_fragment"
113735. .128598
/note="assembly_fragment"
128699. .149705
/note="assembly_fragment"
149806. .151535
/note="assembly_fragment
clone_end:T7
vector_side:right"
BASE COUNT 44763 a 29429 c 29282 g 45460 t 2601 others
ORIGIN

```

```

Query Match 71.9%; Score 23; DB 2; Length 151535;
Best Local Similarity 83.9%; Pred. No. 1.5e+02;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

QY 2 AATACACACAATATTATTTGTGTGTATTGA 32

```

||||| ||||| ||||| || ||||| ||
Db 59894 AATATAACACAATATTACTTTTGTGTATGA 59924

```

RESULT 14

AC008254/c

LOCUS

DEFINITION

AC008254

Drosophila melanogaster, chromosome 3R, region 85C-85C, BAC clone

AC008254

BACR02G22, complete sequence.

AC008254.7

GI:12957659

HTG.

KEYWORDS

Drosophila melanogaster.

ORGANISM

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 164982)

REFERENCE

AUTHORS

Celnikier,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H.,

Holt,R.A., Evans,C.A., Gocayne,J.D., Ananides,P.G., Brandon,R.C.,

Rogers,Y., An,H., Baldwin,D., Bazon,J., Beeson,K.Y., Busam,D.A.,

Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,

Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D.,

Ferreira,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A.,

Gonzalez,M., Houch,J., Hoskins,R.A., Hostin,D., Howland,T.J.,

Ibegwan,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A.,

McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J.,

Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B.,

Phouanavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F.,

Stapleton,M., Strong,R., Svirskaas,R., Tector,C., Williams,S.M.,

Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C. 85C

Sequencing of Drosophila chromosome 3R, region 85C-85C

Unpublished

2 (bases 1 to 164982)

TITLE

JOURNAL

REFERENCE

AUTHORS

Celnikier,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,

Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,

Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,

Hoskins,R.A., Houston,K.A., Hummasti,S.K., Karra,K., Kearney,L.,

Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,

Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,

Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,

Svirskaas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and

Rubin,G.M.

Direct Submission

Submitted (30-JUL-1999) Drosophila Genome Center, Lawrence Berkeley

Laboratory, MS 64-121, Berkeley, CA 94720, USA

On Feb 17, 2001 this sequence version replaced gi:70181775.

Sequence submitted by:

Berkeley Drosophila Genome Project

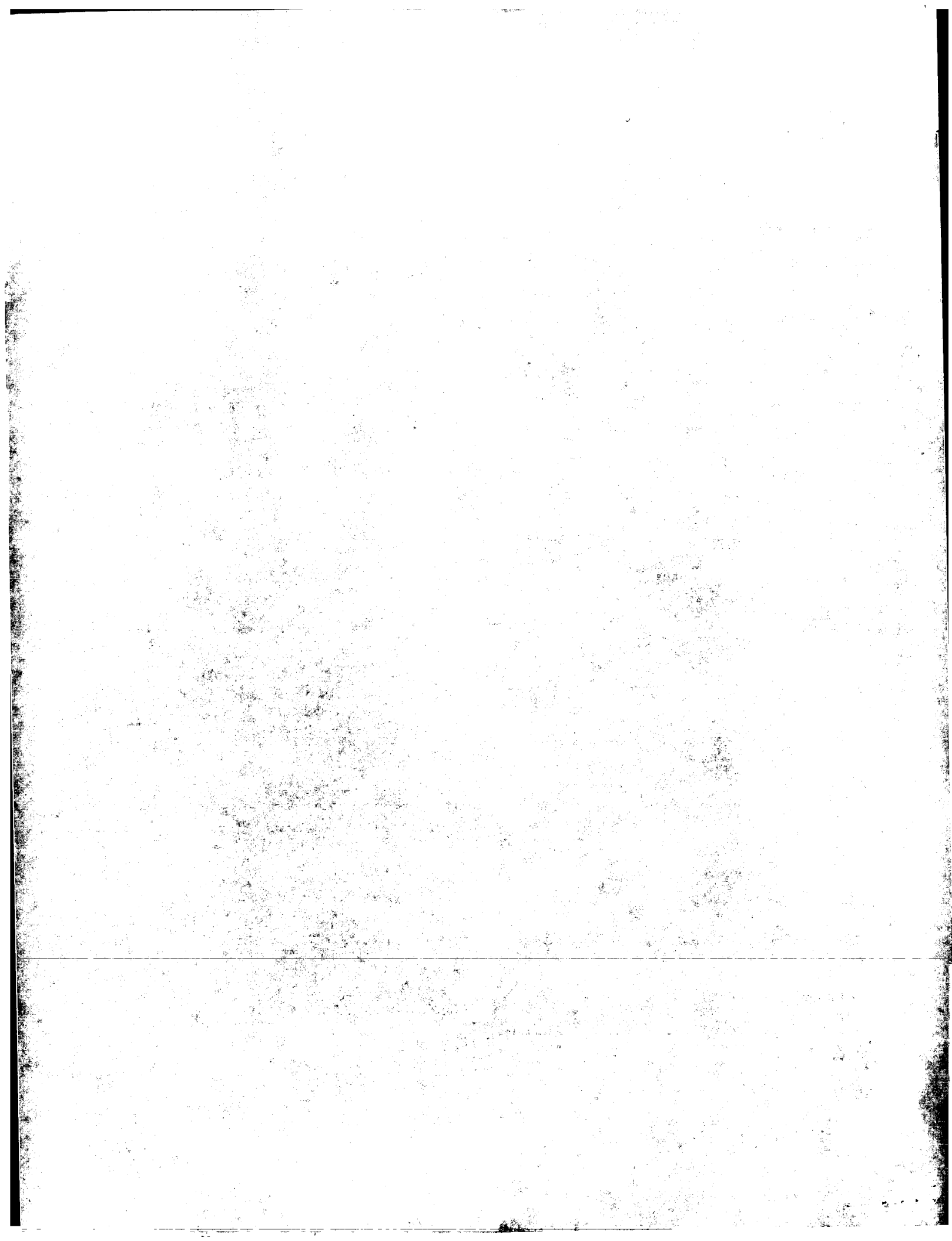
Lawrence Berkeley National Laboratory, MS 64-121

Berkeley, CA 94720

This sequence was assembled using end sequences from a whole genome

shotgun and from subclones of this BAC and its neighboring clones.

For further information about this sequence, including its location



GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2003, 22:30:55 ; Search time 291 Seconds
(without alignments)
247.642 Million cell updates/sec

Title: US-09-895-435-3

Perfect score: 32
Sequence: 1 taataacacacataattgtgtgtatta 32

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_101002:*

- 1: /SID52/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:*
- 2: /SID52/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*
- 3: /SID52/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:*
- 4: /SID52/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*
- 5: /SID52/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:*
- 6: /SID52/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*
- 7: /SID52/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:*
- 8: /SID52/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:*
- 9: /SID52/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:*
- 10: /SID52/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:*
- 11: /SID52/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:*
- 12: /SID52/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:*
- 13: /SID52/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:*
- 14: /SID52/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:*
- 15: /SID52/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:*
- 16: /SID52/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:*
- 17: /SID52/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:*
- 18: /SID52/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:*
- 19: /SID52/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:*
- 20: /SID52/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:*
- 21: /SID52/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:*
- 22: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:*
- 23: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
- 24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	68.8	28360	23 ABL06142	Drosophila melanog
2	21.4	66.9	1112	20 AAK13684	Enterococcus faeca
3	21.4	66.9	12426	22 AAS45482	Tumour suppressor
4	20.8	65.0	434	22 AAK57011	Human immune/haema
5	20.8	65.0	440	22 AAK69305	Human immune/haema
6	20.8	65.0	445	22 AAK66355	Human immune/haema
7	20.8	65.0	445	22 AAK66358	Human immune/haema
8	20.8	65.0	445	22 AAK66496	Human immune/haema
9	20.8	65.0	445	22 AAK66499	Human immune/haema

C 10	20.8	65.0	445	22 AAK69304	Human immune/haema
C 11	20.8	65.0	445	22 AAK69306	Human immune/haema
C 12	20.8	65.0	445	22 AAK69307	Human immune/haema
C 13	20.8	65.0	445	22 AAK84858	Human immune/haema
C 14	20.8	65.0	445	22 AAK84858	Human immune/haema
C 15	20.8	65.0	13377	22 AAS46476	Tumour suppressor
C 16	20.8	65.0	13377	24 ABL33463	Human immune syste
C 17	20.8	65.0	18501	23 ABK43029	Genomic sequence #
C 18	20.8	65.0	335913	22 AAI61371	Soybean 240017 reg
C 19	20.8	65.0	335913	22 AAI61372	Soybean 240017 reg
C 20	20.4	63.7	504	22 AAS28336	Genomic sequence #
C 21	20.4	63.7	504	22 AAS28336	Human immunoglobul
C 22	20.4	63.7	548	22 ABK53294	Human eosinophil-m
C 23	20.4	63.7	1972	22 AAD07834	Human secreted pro
C 24	20.4	63.7	2771	22 AAD07896	Human secreted pro
C 25	20.4	63.7	15141	23 ABL19378	Drosophila melanog
C 26	20.4	63.7	50000	24 ABL56202	Arabidopsis thalia
C 27	20	62.5	1140	21 AAC44850	AmEPV genome fragm
C 28	20	62.5	36445	23 ABL18116	Drosophila melanog
C 29	19.8	61.9	335	24 ABN18845	Human ORFX polynuc
C 30	19.8	61.9	471	22 AAS09349	Rat sequence diffe
C 31	19.8	61.9	562	24 ABK62832	Pneumocystis carin
C 32	19.8	61.9	621	12 AAK12598	Human colon cancer
C 33	19.8	61.9	760	21 AAA01825	Pneumocystis carin
C 34	19.8	61.9	891	13 AAK31427	P.carinii dihydrof
C 35	19.8	61.9	892	12 AAK11961	Human polynucleoti
C 36	19.8	61.9	1936	22 AAI58011	Human ovarian anti
C 37	19.8	61.9	2291	24 ABQ55062	Human secreted pro
C 38	19.8	61.9	2776	20 AAX00678	Human polynucleoti
C 39	19.8	61.9	2833	22 AAI59797	Chromosome 13q31-q
C 40	19.8	61.9	3001	21 AAH51783	Human immune syste
C 41	19.8	61.9	5945	24 ABL32084	Drosophila melanog
C 42	19.8	61.9	6337	23 ABL24528	Drosophila melanog
C 43	19.8	61.9	8477	23 ABL03628	Chemically pretrea
C 44	19.8	61.9	8801	22 AAS45436	Human immune syste
C 45	19.8	61.9	8801	24 ABL33740	

ALIGNMENTS

RESULT 1
ABL06142
ID ABL06142 standard; cDNA; 28360 BP.
XX ABL06142;
AC ABL06142;
DT 26-MAR-2002 (first entry)
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 12908.
DE Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX Drosophila melanogaster.
OS Drosophila melanogaster.
PN WO200171042-A2.
XX 27-SEP-2001.
PD 27-SEP-2001.
PF 23-MAR-2001; 2001WO-US09231.
XX 23-MAR-2001; 2001WO-US09231.
PR 23-MAR-2000; 2000US-191637P.
FR 11-JUL-2000; 2000US-0614150.
XX (PEKE) PE CORP NY.
PA Venter JC, Adams M, Li PWD, Myers EW;
PI WPI; 2001-656860/75.
XX P-PSDB; ABB62039.
DR New isolated nucleic acid detection reagent for detecting 1000 or more
XX

genes from *Drosophila* and for elucidating cell signalling and cell-cell interactions -

Claim 1; SEQ ID NO 12908; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from *Drosophila*. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL61175), expressed DNA sequences (ABL01840-ABL61175) and the encoded proteins (ABB57737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 28360 BP; 7506 A; 6320 C; 6593 G; 7951 T; 0 other;

Query Match 68.8%; Score 22; DB 23; Length 28360;
Best Local Similarity 83.3%; Pred. No. 81;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 TAATACACACATATTAATGTGTTGTAT 30
||| ||||| | ||||| ||||| |||||
13709 TAAACAACAGCTATTTCATTTGGTGTAT 13738

RESULT 2

AAAX13684/C
ID ID AAAX13684 standard; DNA; 1112 BP.

XX
XX AAAX13684;
XX
XX
XX 19-MAR-1999 (first entry)
XX
XX Enterococcus faecalis genome contig SEQ ID NO:747.
XX
XX Enterococcus faecalis; contig; detection; Enterococcal infection;
XX vaccine; attenuation; computer readable medium; ds.
XX
XX Enterococcus faecalis.
XX
XX WO98050555-A2.
XX
XX 12-NOV-1998.
XX
XX
XX 04-MAY-1998; 98WO-US08985.
XX
XX 14-NOV-1997; 97US-0066009.
XX 06-MAY-1997; 97US-0044031.
XX 16-MAY-1997; 97US-0046655.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Barash SC, Dillon PJ, Kunsch CA;
XX
XX WPI; 1999-045171/04.
XX
XX New isolated Enterococcus faecalis polynucleotides and polypeptides
XX - used to develop products for the detection of Enterococcus and for
XX use in vaccines for prevention or attenuation of Enterococcus
XX infection.
XX
XX
XX Claim 1; Page 1964-1965; 2084pp; English.

A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAAX12938 to AAAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for


```
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 29-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-024617.
PR 08-NOV-2000; 2000US-0246174.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.

PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Rosen CA, Barash SC, Ruben SM;
XX
XX DR WPI; 2001-483426/52.
XX
XX PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX PT useful for preventing, diagnosing and/or treating cancers and
XX PT metastasis -
XX
PS Disclosure: SEQ ID NO 24117; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 440 BP; 140 A; 109 C; 94 G; 97 T; 0 other;

Query Match 65.0%; Score 20.8; DB 22; Length 440;
Best Local Similarity 91.7%; Pred. No. 2.2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATACAACACAAATATTAAATGTGTT 26
||||| ||||| ||||| |||||
Db 235 ATACAACACAAATGAATGTGTT 212

RESULT 6
AAK66355
ID AAK66355 standard; DNA; 445 BP.
XX
AC AAK66355;
XX
XX 06-NOV-2001 (first entry)
DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:21167.
XX
XX Human; immune; hematopoietic; immune/hematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
```

XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-02114886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216680.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225347.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 23-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 08-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241789.
PR 20-OCT-2000; 2000US-0241789.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX

PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249266.
PR 17-NOV-2000; 2000US-0249267.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
PA (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-483426/52.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX Disclosure; SEQ ID NO 21170; 3071pp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AM82170 to AM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting

CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
XX
SQ Sequence 445 BP; 98 A; 94 C; 112 G; 141 T; 0 other;

Query Match 65.0%; Score 20.8; DB 22; Length 445;
Best Local Similarity 91.7%; Pred. No. 2.2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATACAACACACATATTAATTGTGTT 26
Db 211 ATACAACACACAAATGAATGTGTT 234

RESULT 8
AAK66496
ID AAK66496 standard; DNA; 445 BP.
XX AC
XX AAK66496;
XX
XX 06-NOV-2001 (first entry)
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21308.
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytotstatic; gene therapy; vaccine; metastasis; ds.
KW
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
XX 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225477.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.

AAK66499
ID AAK66499 standard; DNA; 445 BP.
AC AAK66499;
XX
XX
DT 06-NOV-2001 (first entry)
XX
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21311.
XX
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
KW
XX Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01354.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 28-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.


```
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-025179.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
XX Disclosure; SEQ ID NO 21311; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
XX amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patients own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/haematopoietic-related diseases, especially
XX cancers and cancer metastases of haematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/haematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAM82169
XX represent sequences used in the exemplification of the present invention.
XX
XX SQ Sequence 445 BP; 98 A; 94 C; 112 G; 141 T; 0 other;

Query Match 65.0%; Score 20.8; DB 22; Length 445;
Best Local Similarity 91.7%; Pred. No. 2.2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATACACACAAATATTATTGTT 26
Db ||||||||| |||||||||
211 ATACACACAAATGATTGTT 234

RESULT 10
AAK69304/c
ID AAK69304 standard; DNA; 445 BP.
XX
XX AC AAK69304;
XX
XX DT 06-NOV-2001 (first entry)
XX
XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24116.
XX
XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200157182-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 17-JAN-2001; 2001WO-US01354.
XX
XX
```

```
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
```

PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 20-OCT-2000; 2000US-0241827.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249219.
PR 17-NOV-2000; 2000US-0249220.
PR 17-NOV-2000; 2000US-0249224.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

PR (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-483426/52.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
DR useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
PT

XX Disclosure; SEQ ID NO 24116; 3071pp + Sequence Listing; English.
PS AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
XX Sequence 445 BP; 141 A; 112 C; 94 G; 98 T; 0 other;

Query Match 65.0%; Score 20.8; DB 22; Length 445;
Best Local Similarity 91.7%; Pred. No. 2.2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATACACACAAATATTATTGTTGTT 26
|||||
Db 235 ATACACACAAATGAATTGTTGTT 212
|||||

RESULT 11
AAK69306/c
ID AAK69306 standard; DNA; 445 BP.
XX AC AAK69306;
XX DT 06-NOV-2001 (first entry)
XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24118.
XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX OS Homo sapiens.
XX PN WO200157182-A2.
XX PD 09-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01354.
XX PR 31-JAN-2000; 2000US-0179065.
XX PR 04-FEB-2000; 2000US-0180628.
XX PR 24-FEB-2000; 2000US-0184664.
XX PR 02-MAR-2000; 2000US-0186350.
XX PR 16-MAR-2000; 2000US-0189874.
XX PR 17-MAR-2000; 2000US-0190076.
XX PR 18-APR-2000; 2000US-0198123.
XX PR 19-MAY-2000; 2000US-0205515.
XX PR 07-JUN-2000; 2000US-0209467.
XX PR 28-JUN-2000; 2000US-0214886.
XX PR 30-JUN-2000; 2000US-0215135.
XX PR 07-JUL-2000; 2000US-0216647.
XX PR 07-JUL-2000; 2000US-0216880.
XX PR 11-JUL-2000; 2000US-0217487.
XX PR 11-JUL-2000; 2000US-0217496.
XX PR 14-JUL-2000; 2000US-0218290.
XX PR 26-JUL-2000; 2000US-0220963.
XX PR 26-JUL-2000; 2000US-0220964.
XX PR 14-AUG-2000; 2000US-0224518.
XX PR 14-AUG-2000; 2000US-0224519.


```
XX
SQ      Sequence 445 BP; 141 A; 112 C; 94 G; 98 T; 0 other;
      Query Match      65.0%; Score 20.8; DB 22; Length 445;
      Best Local Similarity 91.7%; Pred. No. 2.2e+02;
      Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 ATACACACAATATTAAATGTTT 26
      |||||
Db      235 ATACACACAAAATGAATTGTTT 212

RESULT 12
AAK69307/c
ID      AAK69307 standard; DNA; 445 BP.
XX
XX      AAK69307;
XX
XX      06-NOV-2001 (first entry)
XX      Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24119.
XX
XX      Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX      cytostatic; gene therapy; vaccine; metastasis; ds.
XX      Homo sapiens.
XX      WO200157182-A2.
XX
XX      09-AUG-2001.
XX
XX      17-JAN-2001; 2001WO-US01354.
XX
XX      31-JAN-2000; 2000US-0179065.
XX      04-FEB-2000; 2000US-0180628.
XX      24-FEB-2000; 2000US-0184664.
XX      02-MAR-2000; 2000US-0186350.
XX      16-MAR-2000; 2000US-0189874.
XX      17-MAR-2000; 2000US-0190076.
XX      18-MAR-2000; 2000US-0198123.
XX      19-MAY-2000; 2000US-0205515.
XX      07-JUN-2000; 2000US-0209467.
XX      30-JUN-2000; 2000US-0215135.
XX      28-JUN-2000; 2000US-0214886.
XX      07-JUL-2000; 2000US-0216647.
XX      07-JUL-2000; 2000US-0216880.
XX      11-JUL-2000; 2000US-0217487.
XX      11-JUL-2000; 2000US-0217496.
XX      14-JUL-2000; 2000US-0218290.
XX      26-JUL-2000; 2000US-0220963.
XX      26-JUL-2000; 2000US-0220964.
XX      14-AUG-2000; 2000US-0224518.
XX      14-AUG-2000; 2000US-0224519.
XX      14-AUG-2000; 2000US-0225213.
XX      14-AUG-2000; 2000US-0225214.
XX      14-AUG-2000; 2000US-0225266.
XX      14-AUG-2000; 2000US-0225267.
XX      14-AUG-2000; 2000US-0225268.
XX      14-AUG-2000; 2000US-0225270.
XX      14-AUG-2000; 2000US-0225447.
XX      14-AUG-2000; 2000US-0225757.
XX      14-AUG-2000; 2000US-0225758.
XX      14-AUG-2000; 2000US-0225759.
XX      18-AUG-2000; 2000US-0226279.
XX      22-AUG-2000; 2000US-0226681.
XX      22-AUG-2000; 2000US-0226688.
XX      22-AUG-2000; 2000US-0227182.
XX      23-AUG-2000; 2000US-0227009.
XX      30-AUG-2000; 2000US-0228924.
XX      01-SEP-2000; 2000US-0229287.
XX      01-SEP-2000; 2000US-0229343.
XX      01-SEP-2000; 2000US-0229344.
XX      01-SEP-2000; 2000US-0229345.
XX      05-SEP-2000; 2000US-0229509.
XX      05-SEP-2000; 2000US-0229513.
XX      06-SEP-2000; 2000US-0230437.
XX      06-SEP-2000; 2000US-0230438.
XX      08-SEP-2000; 2000US-0231242.
XX      08-SEP-2000; 2000US-0231243.
XX      08-SEP-2000; 2000US-0231244.
XX      08-SEP-2000; 2000US-0231413.
XX      08-SEP-2000; 2000US-0231414.
XX      08-SEP-2000; 2000US-0232080.
XX      08-SEP-2000; 2000US-0232081.
XX      12-SEP-2000; 2000US-0231988.
XX      14-SEP-2000; 2000US-0232397.
XX      14-SEP-2000; 2000US-0232398.
XX      14-SEP-2000; 2000US-0232399.
XX      14-SEP-2000; 2000US-0232400.
XX      14-SEP-2000; 2000US-0232401.
XX      14-SEP-2000; 2000US-0233063.
XX      14-SEP-2000; 2000US-0233064.
XX      14-SEP-2000; 2000US-0233065.
XX      21-SEP-2000; 2000US-0234223.
XX      21-SEP-2000; 2000US-0234274.
XX      25-SEP-2000; 2000US-0234997.
XX      25-SEP-2000; 2000US-0234998.
XX      26-SEP-2000; 2000US-0235484.
XX      27-SEP-2000; 2000US-0235834.
XX      27-SEP-2000; 2000US-0235836.
XX      29-SEP-2000; 2000US-0236327.
XX      29-SEP-2000; 2000US-0236367.
XX      29-SEP-2000; 2000US-0236368.
XX      29-SEP-2000; 2000US-0236369.
XX      29-SEP-2000; 2000US-0236370.
XX      02-OCT-2000; 2000US-0236802.
XX      02-OCT-2000; 2000US-0237037.
XX      02-OCT-2000; 2000US-0237038.
XX      02-OCT-2000; 2000US-0237039.
XX      02-OCT-2000; 2000US-0237040.
XX      13-OCT-2000; 2000US-0239935.
XX      13-OCT-2000; 2000US-0239937.
XX      20-OCT-2000; 2000US-0240960.
XX      20-OCT-2000; 2000US-0241221.
XX      20-OCT-2000; 2000US-0241785.
XX      20-OCT-2000; 2000US-0241786.
XX      20-OCT-2000; 2000US-0241787.
XX      20-OCT-2000; 2000US-0241808.
XX      20-OCT-2000; 2000US-0241809.
XX      20-OCT-2000; 2000US-0241826.
XX      01-NOV-2000; 2000US-0244517.
XX      08-NOV-2000; 2000US-0246474.
XX      08-NOV-2000; 2000US-0246475.
XX      08-NOV-2000; 2000US-0246476.
XX      08-NOV-2000; 2000US-0246477.
XX      08-NOV-2000; 2000US-0246478.
XX      08-NOV-2000; 2000US-0246523.
XX      08-NOV-2000; 2000US-0246524.
XX      08-NOV-2000; 2000US-0246525.
XX      08-NOV-2000; 2000US-0246526.
XX      08-NOV-2000; 2000US-0246527.
XX      08-NOV-2000; 2000US-0246528.
XX      08-NOV-2000; 2000US-0246532.
XX      08-NOV-2000; 2000US-0246609.
XX      08-NOV-2000; 2000US-0246610.
XX      08-NOV-2000; 2000US-0246611.
XX      08-NOV-2000; 2000US-0246613.
XX      17-NOV-2000; 2000US-0249207.
XX      17-NOV-2000; 2000US-0249208.
XX      17-NOV-2000; 2000US-0249209.
XX      17-NOV-2000; 2000US-0249210.
XX      17-NOV-2000; 2000US-0249211.
XX      17-NOV-2000; 2000US-0249212.
XX      17-NOV-2000; 2000US-0249213.
XX      17-NOV-2000; 2000US-0249214.
XX      17-NOV-2000; 2000US-0249215.
```



```

PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239035.
PR 13-OCT-2000; 2000US-0239037.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249219.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249267.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX Disclosure; SEQ ID NO 39670; 3071pp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patient's own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting the
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/hematopoietic-related diseases, especially
XX cancers and cancer metastases of haematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/hematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAK82169
XX represent sequences used in the exemplification of the present invention.
XX SQ Sequence 445 BP; 98 A; 94 C; 112 G; 141 T; 0 other;
Query Match 65.0%; Score 20.8; DB 22; Length 445;
Best Local Similarity 91.7%; Pred. NO. 2.2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 ATACACACAAATATTAAATGTGTT 26
Db 211 ATACACACAAATGAATGTGTT 234
RESULT 14
AAK84862
ID AAK84862 standard; DNA; 445 BP.
XX AAK84862;
AC AAK84862;
XX
XX 07-NOV-2001 (first entry)
XX Human immune/hematopoietic antigen genomic sequence SEQ ID NO:39674.
XX Human; immune; haematopoietic; immune/hematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
XX Homo sapiens.
XX WO200157182-A2.
XX
XX 09-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01354.
XX
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
```

PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249266.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-483426/52.
Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
useful for preventing, diagnosing and/or treating cancers and
metastasis -
Disclosure; SEQ ID NO 39674; 3071pp + Sequence Listing; English.
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAK62170 to AAK91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and

CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 445 BP; 98 A; 94 C; 112 G; 141 T; 0 other;

Query Match 65.0%; Score 20.8; DB 22; Length 445;
 Best Local Similarity 91.7%; Pred. No. 2.2e-02;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATACAACACAATTAATTGTTGTT 26
 ||||| ||||| ||||| ||||| |||||
 Db 211 ATACAACACAATGAATGTTGTT 234

RESULT 15
 AAS46476
 ID AAS46476 standard; DNA; 13377 BP.
 XX
 AC AAS46476;
 XX

DT 18-DEC-2001 (first entry)
 XX
 DE Tumour suppressor gene derived chemically modified sequence #198.
 XX
 KW Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
 KW cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
 KW cytosine methylation; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200168912-A2.
 PN
 PD 20-SEP-2001.
 XX
 XX 15-MAR-2001; 2001WO-EP02955.
 XX
 XX 15-MAR-2000; 2000DE-1013847.
 PR
 PR 06-APR-2000; 2000DE-1019058.
 PR
 PR 07-APR-2000; 2000DE-1019173.
 PR
 PR 30-JUN-2000; 2000DE-1032529.
 PR
 PR 01-SEP-2000; 2000DE-1043826.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 PA

XX Olek A, Piepenbrock C, Berlin K;
 PI
 XX WPI; 2001-602752/68.
 DR
 XX
 XX Fragments of chemically modified genes associated with tumour suppressor
 PT genes and oncogenes, useful in designing primers and probes for
 PT analysing diseases associated with cytosine methylation state e.g.
 PT cancer -
 PT
 XX Claim 1; SEQ ID NO 198; 27pp; English.
 PS
 XX

CC The invention relates to a nucleic acid comprising a sequence of 18
 CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
 CC bisulphite, of genes associated with tumour suppression and
 CC oncogenes having a sequence taken from 536 (actually 533 since
 CC numbers 408, 458 and 500 are missing from the sequence listing) sequences
 CC (SS) and sequences complementary to (SS). The nucleic acid may be a
 CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may

CC form part of a set of probes for detecting the cytosine methylation state
 CC and/or single nucleotide polymorphisms and also to be used in an
 CC array for analysing diseases associated with CpG dinucleotides e.g.
 CC cancers and tumours. The probes can also be used in a method for
 CC ascertaining genetic and/or epigenetic parameters for the diagnosis
 CC and/or therapy of existing diseases or the predisposition to specific
 CC diseases, by analysing cytosine methylations. The parameters may be
 CC compared to another set of genetic and/or epigenetic parameters, the
 CC differences serving as basis for diagnosis and/or prognosis events which
 CC are disadvantageous to patients. The present sequence is one of the
 CC 533 genomic sequences derived from tumour suppressor genes and
 CC oncogenes. Sequences with even numbered Seq ID numbers are the
 CC complementary sequence of the corresponding odd numbered sequence (e.g.
 CC ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence
 CC is missing).
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 13377 BP; 3714 A; 146 C; 2702 G; 6815 T; 0 other;

Query Match 65.0%; Score 20.8; DB 22; Length 13377;
 Best Local Similarity 78.1%; Pred. No. 2.1e-02;
 Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TAATACACACAAATTAATTGTTGTATTA 32
 | | | | | | | | | | | | | | | | | | | | | |
 Db 5498 TTATATAAAGAATTAATTACGTGGTATTA 5529

Search completed: February 13, 2003, 01:45:42
 Job time : 300 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 13, 2003, 01:38:51 ; Search time 66 Seconds
(without alignments)
148.692 Million cell updates/sec

Title: US-09-895-435-3
Perfect score: 32
Sequence: 1 taatacacacaataattgtgtgattatta 32

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19.8	61.9	891	6	Patent No. 5164490-2
2	19.2	60.0	36	3	US-08-770-941-13
3	19.2	60.0	342	4	US-09-134-001C-2702
4	19.2	60.0	360	3	US-08-935-263-17
5	19.2	60.0	360	4	US-09-594-185-17
6	18.8	58.8	266	2	US-08-687-080-86
7	18.8	58.8	564	4	US-08-984-320-1
8	18.8	58.8	564	4	US-08-487-087A-1
9	18.8	58.8	564	4	US-08-397-653B-1
10	18.8	58.8	564	6	5175095-1
11	18.8	58.8	2132	3	US-08-844-188-39
12	18.8	58.8	2132	4	US-09-378-088A-39
13	18.8	58.8	3528	4	US-08-984-320-2
14	18.8	58.8	3528	4	US-08-487-087A-2
15	18.8	58.8	4383	4	US-08-397-653B-2
16	18.8	58.8	4383	6	5175095-4
17	18.8	58.8	4383	6	5177307-1
18	18.8	58.8	4833	4	US-09-066-047-1
19	18.6	58.1	3155	2	US-08-591-629-7
20	18.6	58.1	168575	4	US-09-426-290-1
21	18.4	57.5	3561	1	US-08-485-568A-3
22	18.4	57.5	3561	1	US-08-357-698-5
23	18.4	57.5	3561	2	US-08-590-554A-3
24	18.4	57.5	3561	2	US-09-184-223-3
25	18.4	57.5	3561	5	PCT-US93-12682-5
26	18.4	57.5	4435	1	US-08-308-872B-5
27	18.2	56.9	1107	4	US-09-173-300-50

28	18.2	56.9	1483	1	US-07-966-187-11	Sequence 11, Appl
29	18.2	56.9	1483	1	US-07-966-187-13	Sequence 13, Appl
30	18.2	56.9	2301	4	US-09-561-825-1	Sequence 1, Appl
31	18.2	56.9	2361	4	US-09-561-825-26	Sequence 26, Appl
32	18.2	56.9	2361	4	US-09-561-825-29	Sequence 29, Appl
33	18.2	56.9	2361	4	US-09-561-825-27	Sequence 27, Appl
34	18.2	56.9	2363	4	US-09-561-825-28	Sequence 28, Appl
35	18.2	56.9	6343	3	US-08-581-148C-30	Sequence 30, Appl
36	18.2	56.9	11721	4	US-09-026-039-3	Sequence 3, Appl
37	18.2	56.9	11721	4	US-09-026-039-3	Sequence 3, Appl
38	18	56.2	652	4	US-08-936-165A-105	Sequence 105, App
39	18	56.2	712	1	US-08-410-804-4	Sequence 4, Appl
40	18	56.2	712	1	US-08-259-514-4	Sequence 4, Appl
41	18	56.2	712	2	US-08-858-311-4	Sequence 4, Appl
42	18	56.2	747	1	US-08-680-726A-87	Sequence 87, Appl
43	18	56.2	747	3	US-09-092-408-87	Sequence 87, Appl
44	18	56.2	749	1	US-08-680-726A-85	Sequence 85, Appl
45	18	56.2	749	1	US-08-680-726A-86	Sequence 86, Appl

ALIGNMENTS

RESULT 1
5164490-2
; Patent No. 5164490
; APPLICANT: SANTU, DANIEL V.;EDMAN, JEFFREY;EDMAN, URSULA
; TITLE OF INVENTION: PNEUMOCYSTIS CARINII DIHYDROFOLATE
; REDUCTASE GENE AND METHODS FOR ITS USE
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/437,511
; FILING DATE: 15-NOV-1989
; SEQ ID NO:2:
; LENGTH: 891
5164490-2

Query Match 61.9%; Score 19.8; DB 6; Length 891;
Best Local Similarity 77.4%; Pred. No. 48;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TAATACACACAATATTATTTGTTGTATT 31
||||| - ||||| ||||| |||||
Db 507 TAATATACAGGATTCATTTGTGATGATT 537

RESULT 2
US-08-770-941-13
; Sequence 13, Application US/08770941
; Patent No. 6025133
; GENERAL INFORMATION:
; APPLICANT: Stull, Paul D.
; APPLICANT: Myers, Kristi K.
; APPLICANT: Becker, Michael M.
; TITLE OF INVENTION: TARGET-TRIGGERED
; TITLE OF INVENTION: AMPLIFICATION
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,941

```

; CURRENT APPLICATION NUMBER: US/08/935,263A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: EP 96115540.5
; EARLIER FILING DATE: 1996-09-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Kurthia sp.
; FEATURE:
; NAME/KEY: RBS
; LOCATION: Complement((67)..(76))
; FEATURE:
; NAME/KEY: -35_signal
; LOCATION: (210)..(215)
; FEATURE:
; NAME/KEY: -10_signal
; LOCATION: (234)..(239)
; FEATURE:
; NAME/KEY: -10_signal
; LOCATION: Complement((235)..(240))
; FEATURE:
; NAME/KEY: RBS
; LOCATION: (289)..(293)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (302)..(358)
; OTHER INFORMATION: Partial sequence of ORF2.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (125)..(164)
; OTHER INFORMATION: BOX1 - inverted repeat
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (244)..(293)
; OTHER INFORMATION: BOX2 - inverted repeat
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((1)..(58))
; OTHER INFORMATION: Partial sequence of ORF1.
;
US-08-935-263-17

Query Match          60.0%; Score 19.2; DB 3; Length 360;
Best Local Similarity 75.0%; Pred. No. 80;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TAATACACACAATATTAAATTGTGTGTATTA 32
    ||||| ||||| || ||||| |||||
Db 207 TAATTGAACAATATTTATTGTGTGTATTA 238

RESULT 5
US-09-594-185-17
; Sequence 17, Application US/09594185
; Patent No. 6365388
; GENERAL INFORMATION:
; APPLICANT: Furuichi, Yasuhiro
; APPLICANT: Hoshino, Tatsuo
; APPLICANT: Kimura, Hitoshi
; APPLICANT: Kiyasu, Tatsuya
; APPLICANT: Nagahashi, Yoshie
; TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
; FILE REFERENCE: Biotin Genes
; CURRENT APPLICATION NUMBER: US/09/594,185
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 08/935,263
; PRIOR FILING DATE: 1997-09-22
; PRIOR APPLICATION NUMBER: EP 96115540.5
; PRIOR FILING DATE: 1996-09-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17

```

```
;
;
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Kurthia sp.
; FEATURE:
; NAME/KEY: RBS
; LOCATION: Complement((67)..(76))
; NAME/KEY: -35_signal
; LOCATION: (210)..(215)
; NAME/KEY: -10_signal
; LOCATION: (234)..(239)
; NAME/KEY: -10_signal
; LOCATION: Complement((235)..(240))
; NAME/KEY: RBS
; LOCATION: (289)..(293)
; NAME/KEY: misc_feature
; LOCATION: (302)..(358)
; OTHER INFORMATION: Partial sequence of ORF2.
; NAME/KEY: misc_feature
; LOCATION: (125)..(164)
; OTHER INFORMATION: BOX1 - inverted repeat
; NAME/KEY: misc_feature
; LOCATION: (244)..(283)
; OTHER INFORMATION: BOX2 - inverted repeat
; NAME/KEY: misc_feature
; LOCATION: Complement((1)..(58))
; OTHER INFORMATION: Partial sequence of ORF1.
US-09-594-185-17

Query Match      60.0%; Score 19.2; DB 4; Length 360;
Best Local Similarity 75.0%; Pred. No. 80;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TAATACACACATATTAATGTGTTGTTATTA 32
    |||| |||| |||| |||| |||| |||| ||||
Db 207 TAATGAACAATATTTATTTGTTGTTATTA 238

RESULT 6
US-08-687-080-86
; Sequence 86, Application US/08687080
; Patent No. 5965427
; GENERAL INFORMATION:
; APPLICANT: Gregory Dolganov
; TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,080
; FILING DATE: 17-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/592,126
; FILING DATE: 26-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 4600-0111.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 360 base pairs
; TYPE: DNA
; STRANDEDNESS: double
; TOPOLOGY: circular
;
; Molecule Type: cdna to mRNA

;
; LENGTH: 266 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: 3' END OF INTRON 13 OF RAD50 GENOMIC
; INDIVIDUAL ISOLATE: SEQUENCE
US-08-687-080-86

Query Match      58.8%; Score 18.8; DB 2; Length 266;
Best Local Similarity 76.7%; Pred. No. 11e+02;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 AATACACACATATTAATGTGTTGTTATT 31
    || |||| |||| || |||| |||| ||||
Db 160 AAAAGAACACAAATGTCACCTTCTGTGTATT 189

RESULT 7
US-08-984-320-1/c
; Sequence 1, Application US/08984320
; Patent No. 6222097
; GENERAL INFORMATION:
; APPLICANT: McBride, Kevin E.
; APPLICANT: Stalker, David M.
; TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: CA
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 Inch, 1.4 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1 (a)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/984,320
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,087
; FILING DATE: 07-JUN-95
; APPLICATION NUMBER: USSN 07/998,158
; FILING DATE: 29-DEC-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 07/554,195
; FILING DATE: 17-JUL-90
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 07/382,518
; FILING DATE: 19-JUL-89
; ATTORNEY/AGENT INFORMATION:
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; NAME: Carl J. Schwedler
; REGISTRATION NUMBER: 36,924
; REFERENCE/DOCKET NUMBER: CGNE 91-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 564 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
```

US-08-984-320-1					
Query Match 58.8%; Score 18.8; DB 4; Length 564;					
Best Local Similarity 76.7%; Pred. No. 1.le+02;					
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;					
QY	2	AATACACACAATAATTGTTGTATT	31		
Db	423	AAGCAACACTTATTAAATTTGGTTTTT	394		
RESULT 8					
US-08-487-087A-1/c					
Sequence 1, Application US/08487087A					
Patent No. 6268546					
GENERAL INFORMATION:					
APPLICANT: McBride, Kevin E.					
TITLE OF INVENTION: Stalker, David M.					
NUMBER OF SEQUENCES: 6					
CORRESPONDENCE ADDRESS:					
ADDRESSEE: Calgene, Inc.					
STREET: 1920 Fifth Street					
CITY: Davis					
STATE: CA					
COUNTRY: USA					
ZIP: 95616					
COMPUTER READABLE FORM:					
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB					
COMPUTER: Apple Macintosh					
OPERATING SYSTEM: Macintosh 7.1					
SOFTWARE: Microsoft Word 5.1 (a)					
CURRENT APPLICATION DATA:					
APPLICATION NUMBER: US/08/487,087A					
FILING DATE: 07-JUN-95					
CLASSIFICATION: 800					
PRIOR APPLICATION DATA:					
APPLICATION NUMBER: USSN 07/998,158					
FILING DATE: 29-DEC-92					
PRIOR APPLICATION DATA:					
APPLICATION NUMBER: USSN 07/554,195					
FILING DATE: 17-JUL-90					
PRIOR APPLICATION DATA:					
APPLICATION NUMBER: USSN 07/382,518					
FILING DATE: 19-JUL-89					
ATTORNEY/AGENT INFORMATION:					
NAME: Donna E. Scherer					
REGISTRATION NUMBER: 34,719					
NAME: Carl J. Schwedler					
REGISTRATION NUMBER: 36,924					
REFERENCE/DOCKET NUMBER: CGNE 91-1					
TELECOMMUNICATION INFORMATION:					
TELEPHONE: (916) 753-6313					
TELEFAX: (916) 753-1510					
INFORMATION FOR SEQ ID NO: 1:					
SEQUENCE CHARACTERISTICS:					
LENGTH: 564 base pairs					
TYPE: nucleic acid					
STRANDEDNESS: double					
TOPOLOGY: linear					
MOLECULE TYPE: cdna to mRNA					
US-08-487-087A-1					
Query Match 58.8%; Score 18.8; DB 4; Length 564;					
Best Local Similarity 76.7%; Pred. No. 1.le+02;					
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;					
QY	2	AATACACACAATAATTGTTGTATT	31		
Db	423	AAGCAACACTTATTAAATTTGGTTTTT	394		
RESULT 9					
US-08-397-653B-1/c					
Sequence 1, Application US/08397653B					
Patent No. 6329570					
GENERAL INFORMATION:					
APPLICANT: Martineau, Belinda					
TITLE OF INVENTION: COTTON MODIFICATION USING					
OVAR-TISSUE TRANSCRIPTIONAL					
FACTORS					
NUMBER OF SEQUENCES: 10					
CORRESPONDENCE ADDRESS:					
ADDRESSEE: Calgene, Inc.					
STREET: 1920 Fifth Street					
CITY: Davis					
STATE: CA					
COUNTRY: USA					
ZIP: 95616					
COMPUTER READABLE FORM:					
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB					
COMPUTER: Apple Macintosh					
OPERATING SYSTEM: Macintosh 7.0					
SOFTWARE: Microsoft Word 5.1a					
CURRENT APPLICATION DATA:					
APPLICATION NUMBER: US/08/397,653B					
FILING DATE: 28-FEB-1995					
CLASSIFICATION: 800					
ATTORNEY/AGENT INFORMATION:					
NAME: Elizabeth Lassen					
REGISTRATION NUMBER: 31,845					
NAME: Donna E. Scherer					
REGISTRATION NUMBER: 34,719					
NAME: Carl J. Schwedler					
REGISTRATION NUMBER: 36,924					
REFERENCE/DOCKET NUMBER: CGNE 112					
TELECOMMUNICATION INFORMATION:					
TELEPHONE: (916) 753-6313					
TELEFAX: (916) 753-1510					
INFORMATION FOR SEQ ID NO: 1:					
SEQUENCE CHARACTERISTICS:					
LENGTH: 564 base pairs					
TYPE: nucleic acid					
STRANDEDNESS: single					
TOPOLOGY: linear					
MOLECULE TYPE: CDNA TO MRNA					
US-08-397-653B-1					
Query Match 58.8%; Score 18.8; DB 4; Length 564;					
Best Local Similarity 76.7%; Pred. No. 1.le+02;					
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;					
QY	2	AATACACACAATAATTGTTGTATT	31		
Db	423	AAGCAACACTTATTAAATTTGGTTTTT	394		
RESULT 10					
5175095-1/c					
Patent No. 5175095					
APPLICANT: Martineau, Belinda M.; Houck, Catherine M.					
TITLE OF INVENTION: OVARY TISSUE TRANSCRIPTIONAL FACTORS					
NUMBER OF SEQUENCES: 9					
CURRENT APPLICATION DATA:					
APPLICATION NUMBER: US/07/554,195					
FILING DATE: 17-JUL-1990					
SEQ ID NO: 1:					
LENGTH: 564					
5175095-1					
Query Match 58.8%; Score 18.8; DB 6; Length 564;					
Best Local Similarity 76.7%; Pred. No. 1.le+02;					
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;					
QY	2	AATACACACAATAATTGTTGTATT	31		
Db	423	AAGCAACACTTATTAAATTTGGTTTTT	394		

Db 423 AAGCAACACTTTATTAATTTTGTGTTT 394

RESULT 11

US-08-844-188-39/C
; Sequence 39, Application US/08844188
; Patent No. 6127180
; GENERAL INFORMATION:
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Knuth, Mark
; APPLICANT: Pollard, Michael R.
; APPLICANT: Cardineau, Guy
; APPLICANT: Schwab, George E.
; TITLE OF INVENTION: Pesticidal Toxins
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606-6669
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,188
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/633,993
; FILING DATE: 19-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-703C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2132 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-844-188-39

Query Match 58.8%; Score 18.8; DB 3; Length 2132;
Best Local Similarity 76.7%; Pred. No. 1.le+02;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 AATACACACAATTAATTTGTTGTTATT 31
||||| | | | | | | | | | | | | | | |
Db 724 AATACCAAAAATATTTATTTTGGTATT 695

RESULT 12

US-09-378-088A-39/C
; Sequence 39, Application US/09378088A
; Patent No. 6372480
; GENERAL INFORMATION:
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Knuth, Mark
; APPLICANT: Pollard, Michael R.
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Schwab, George E.
; APPLICANT: Michaels, Tracy E.

; APPLICANT: Finstad Lee, Stacy
; APPLICANT: Burmeister, Paula
; APPLICANT: Dojillo, Joanna
; TITLE OF INVENTION: Pesticidal Proteins
; FILE REFERENCE: MA703C2
; CURRENT APPLICATION NUMBER: US/09/378,088A
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: US 08/633,993
; PRIOR FILING DATE: 1996-04-19
; PRIOR APPLICATION NUMBER: US 08/844,188
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 39
; LENGTH: 2132
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-09-378-088A-39

Query Match 58.8%; Score 18.8; DB 4; Length 2132;
Best Local Similarity 76.7%; Pred. No. 1.le+02;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 AATACACACAATTAATTTGTTGTTATT 31
||||| | | | | | | | | | | | | | | |
Db 724 AATACCAAAAATATTTATTTTGGTATT 695

RESULT 13

US-08-984-320-2/C
; Sequence 2, Application US/08984320
; Patent No. 6222097
; GENERAL INFORMATION:
; APPLICANT: McBride, Kevin E.
; APPLICANT: Stalker, David M.
; TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: CA
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1 (a)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/984,320
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,087
; FILING DATE: 07-JUN-95
; APPLICATION NUMBER: USSN 07/998,158
; FILING DATE: 29-DEC-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 07/554,195
; FILING DATE: 17-JUL-90
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 07/382,518
; FILING DATE: 19-JUL-89
; ATTORNEY/AGENT INFORMATION:
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; NAME: Carl J. Schwedler
; REGISTRATION NUMBER: 36,924
; REFERENCE/DOCKET NUMBER: CGNE 91-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510

Query Match 58.8%; Score 18.8; DB 4; Length 3528;
Best Local Similarity 76.7%; Pred. No. 1e+02;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Search completed: February 13, 2003, 04:52:39
Job time : 71 secs

Query Match 58.8%; Score 18.8; DB 4; Length 3528;
Best Local Similarity 76.7%; Pred. NO. 1e+02;
Matches 23; Conservative 0; Mismatches 7; Indels 0

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 13, 2003, 01:41:21 : Search time 37 seconds
(without alignments)
440.496 Million cell updates/sec

Title: US-09-895-435-3

Perfect score: 32

Sequence: I taatacaacaataattgtgtgtatta 32

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 424239 seqs, 254661826 residues

Total number of hits satisfying chosen parameters: 848478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications_NA:*
- 1: /cgn2_5/ptodata/1/pubpna/US07_PUBCOMB.seq:*
 - 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
 - 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
 - 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
 - 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
 - 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
 - 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
 - 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
 - 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
 - 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
 - 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
 - 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
 - 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
 - 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	21.4	66.9	1112	10	US-09-070-927A-747
2	21.4	66.9	2000	9	Sequence 747, App
3	20.8	65.0	1876	9	Sequence 4932, Ap
C 4	20.8	65.0	18501	10	Sequence 4407, Ap
5	20.8	65.0	335913	9	Sequence 1916, Ap
6	20.8	65.0	335913	9	Sequence 2, Appli
7	20.4	63.7	504	10	Sequence 1916, Ap
C 8	20.2	63.1	448	10	Sequence 770, App
9	19.8	61.9	562	10	Sequence 11904, A
10	19.8	61.9	1936	9	Sequence 739, App
11	19.8	61.9	2776	9	Sequence 217, App
12	19.8	61.9	127197	9	Sequence 78, Appl
C 13	19.8	61.9	148567	9	Sequence 1, Appli
C 14	19.8	61.9	148567	10	Sequence 3, Appli
15	19.6	61.3	357	10	Sequence 3, Appli
16	19.6	61.3	502	10	Sequence 56, App
17	19.6	61.3	513509	9	Sequence 19, Appl
C 18	19.4	60.6	267	10	Sequence 4, Appli
19	19.4	60.6	180216	10	Sequence 3174, Ap
					Sequence 6, Appli

20	19.2	60.0	360	12	US-10-033-078-17
C 21	19.2	60.0	374	9	Sequence 17, Appl
C 22	19.2	60.0	26225	10	Sequence 559, App
23	19	59.4	4565	9	Sequence 1276, Ap
C 24	19	59.4	4565	10	Sequence 8, Appli
C 25	19	59.4	4810	9	Sequence 3, Appli
26	19	59.4	25580	10	Sequence 6, Appli
27	19	59.4	302250	10	Sequence 19, Appl
C 28	18.8	58.8	334	10	Sequence 154, App
29	18.8	58.8	564	10	Sequence 674, App
30	18.8	58.8	669	9	Sequence 1, Appli
31	18.8	58.8	669	9	Sequence 137, App
32	18.8	58.8	2000	9	Sequence 1198, Ap
C 33	18.8	58.8	3528	10	Sequence 4906, Ap
34	18.8	58.8	74586	10	Sequence 2, Appli
C 35	18.8	58.8	74586	10	Sequence 3, Appli
36	18.6	58.1	440	10	Sequence 4375, Ap
37	18.6	58.1	591	10	Sequence 3329, A
C 38	18.6	58.1	2000	9	Sequence 3970, Ap
39	18.6	58.1	3029	9	Sequence 102, App
40	18.4	57.5	2004	10	Sequence 196, App
C 41	18.2	56.9	396	10	Sequence 222, App
42	18.2	56.9	418	10	Sequence 2087, App
C 43	18.2	56.9	462	10	Sequence 138, App
44	18.2	56.9	481	10	Sequence 10268, A
45	18.2	56.9	533	10	Sequence 1875, Ap

ALIGNMENTS

RESULT 1

US-09-070-927A-747/c

Sequence 747, Application US/09070927A

Patent No. US20020120116A1

GENERAL INFORMATION:

APPLICANT: Charles A. Kunsch

Patrick J. Dillon

Steven Barash

TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides

NUMBER OF SEQUENCES: 982

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/070,927A

FILING DATE: 04-May-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/046,655

FILING DATE: 1997-05-16

APPLICATION NUMBER: 60/044,031

FILING DATE: 1997-05-06

APPLICATION NUMBER: 60/066,009

FILING DATE: 1997-11-14

ATTORNEY/AGENT INFORMATION:

NAME: Kenley K. Hoover

REGISTRATION NUMBER: 40,302

REFERENCE/DOCKET NUMBER: PB369

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 747:

SEQUENCE CHARACTERISTICS:

Thu Feb 13 12:34:56 2003

us-09-895-435-3.rnpb

```
;
; LENGTH: 1112 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 747:
US-09-070-927A-747

Query Match          66.9%; Score 21.4; DB 10; Length 1112;
Best Local Similarity 80.6%; Pred. No. 65;
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TAATACACACAATATTAATGTTGTTGTTATT 31
   ||| ||||| ||||| ||||| ||||| ||||| ||
Db 692 TAAACAAACAATAATATATATATATGTTGTTT 662

RESULT 2
US-09-938-842A-4932
; Sequence 4932, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; CURRENT FILING DATE: 2001-08-24
; CURRENT APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 4932
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4932

Query Match          66.9%; Score 21.4; DB 9; Length 2000;
Best Local Similarity 80.6%; Pred. No. 64;
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 AATACACACAATATTAATGTTGTTGTTATTA 32
   || ||||| ||||| ||||| ||||| ||||| ||
Db 445 AAACAAACGAATATTAATAGTTGTATGA 475

RESULT 3
US-09-938-842A-4407
; Sequence 4407, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; CURRENT FILING DATE: 2001-08-24
; CURRENT APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
```

```
; SEQ ID NO 4407
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4407

Query Match          65.0%; Score 20.8; DB 9; Length 1876;
Best Local Similarity 78.1%; Pred. No. 1e+02;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TAATACACACAATATTAATGTTGTTGTTATTA 32
   ||| ||||| ||||| ||||| ||||| ||||| ||
Db 295 TAATACAAATCAATCTTATTTGGGATCAATTA 326

RESULT 4
US-09-764-847-1916/C
; Sequence 1916, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1916
; LENGTH: 18501
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (9022)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (9023)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-847-1916

Query Match          65.0%; Score 20.8; DB 10; Length 18501;
Best Local Similarity 78.1%; Pred. No. 97;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TAATACACACAATATTAATGTTGTTGTTATTA 32
   ||| ||||| ||||| ||||| ||||| ||||| ||
Db 17277 TAAATAACACTAAACTAAATGTTGTATAA 17246

RESULT 5
US-09-754-853A-2
; Sequence 2, Application US/09754853A
; Publication No. US20030005491A1
; GENERAL INFORMATION:
; APPLICANT: Hauge, Brian M.
; APPLICANT: Parsons, Jeremy D.
; APPLICANT: Wang, Ming Li
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Soybean Cyst Nematode Resistance
; FILE REFERENCE: 38-10(15810)B
; CURRENT APPLICATION NUMBER: US/09/754,853A
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,880
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 1119
; SEQ ID NO 2
; LENGTH: 335913
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: CDS
```


LENGTH: 562
TYPE: DNA

QY 1 TAATACAACAATATTAAATTGTTGTAT 30

```
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 A1102871
US-09-917-800A-739

Query Match      61.9%; Score 19.8; DB 10; Length 562;
Best Local Similarity 77.4%; Pred. No. 2.2e+02;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY   1 TAATACACACAATAATTAAATGTTGTCTTATT 31
    ||| ||| ||||||||| ||| |||
Db   451 TAGGTCAAAACAATTAATTAATGTCCTTATT 421

RESULT 10
US-10-098-841-217
; Sequence 217, Application US/10098841
; Publication No. US20020197679A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Xu, Chongjun
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Ren, Feiyao
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Dmanac, Radje T.
; TITLE OF INVENTION: NO. US20020197679A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784CIP2
; CURRENT APPLICATION NUMBER: US/10/098,841
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 217
; LENGTH: 1936
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (81)..(752)
; NAME/KEY: misc_feature
; LOCATION: (1)..(1936)
; OTHER INFORMATION: n = a,t,c or g
US-10-098-841-217

Query Match      61.9%; Score 19.8; DB 9; Length 1936;
Best Local Similarity 77.4%; Pred. No. 2.2e+02;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY   1 TAATACACACAATAATTAAATGTTGTCTTATT 31
    ||| ||| ||||||||| ||| |||
Db   1448 TAAATCAATCAATTAATTAATGTCCTTATT 1478

RESULT 11
US-09-984-245-78
; Sequence 78, Application US/09984245
; Patent No. US20020165374A1
```


us-09-895-435-3.rnpb

Thu Feb 13 12:34:56 2003

Db 18 TAATCAACACATATTTCATCGTATT 43

Search completed: February 13, 2003, 04:56:51
Job time : 241 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run On: February 12, 2003, 23:34:41 : Search time 2255 Seconds
(without alignments)
229.825 Million cell updates/sec

Title: US-09-895-435-3
Perfect score: 32
Sequence: 1 taataacacacataattattgtttgtattta 32

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estnu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_hic:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_hic:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estom:*
 - 17: gb_gss:*
 - 18: em_gss_hum:*
 - 19: em_gss_inv:*
 - 20: em_gss_pln:*
 - 21: em_gss_vrt:*
 - 22: em_gss_fun:*
 - 23: em_gss_mam:*
 - 24: em_gss_mus:*
 - 25: em_gss_other:*
 - 26: em_gss_pro:*
 - 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
c 1	24	75.0	953	17	CNS0431LN
c 2	23.6	73.8	510	17	AZ523535
c 3	23.2	72.5	700	17	C19D10
c 4	23	71.9	459	9	AA677944
5	22.8	71.2	1101	17	CNS002SR
6	22.6	70.6	526	9	AA101244

7	22.4	70.0	523	17	AQ970499
c 8	22.4	70.0	562	17	AZ848763
c 9	22.4	70.0	584	14	BQ692893
c 10	22.4	70.0	633	17	AQ450340
11	22	68.8	239	13	BJ365887
12	22	68.8	505	10	AV385246
13	22	68.8	571	17	AQ319355
c 14	21.8	68.1	1042	17	CNS05J05
15	21.6	67.5	536	14	BQ693146
16	21.4	66.9	554	10	AW334296
c 17	21.4	66.9	610	17	BH762639
c 18	21.4	66.9	716	17	BH536105
c 19	21.4	66.9	808	17	BH452731
c 20	21.4	66.9	810	17	BH419970
c 21	21.4	66.9	831	17	BH589798
c 22	21.4	66.9	843	17	BH248522
23	21.4	66.9	850	17	BH161606
24	21.4	66.9	913	17	BH157595
c 25	21.4	66.9	920	17	BH134609
c 26	21.4	66.9	958	17	B08958
c 27	21.4	66.9	1154	17	CNS06PT8
c 28	21	65.6	345	9	AA860018
c 29	21	65.6	484	17	BH741995
30	21	65.6	510	9	A1726715
31	21	65.6	583	9	A1729966
c 32	21	65.6	603	17	PT022K01R
c 33	21	65.6	603	17	AQ662080
c 34	21	65.6	626	9	A1730796
35	21	65.6	630	17	AZ883204
c 36	21	65.6	684	17	BH698214
37	21	65.6	831	12	BC441984
38	21	65.6	1007	17	CNS02W13
39	21	65.6	1070	17	CNS03PL2
40	21	65.6	1130	12	BG033546
41	20.8	65.0	281	13	BI883362
42	20.8	65.0	303	17	AQ005284
c 43	20.8	65.0	318	17	B54164
c 44	20.8	65.0	342	10	AV559105
c 45	20.8	65.0	402	10	AW464877

ALIGNMENTS

RESULT 1
CNS0431LN/c
LOCUS
DEFINITION

CNS0431LN 953 bp DNA linear GSS 18-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-Ori end of Clone
079N02 of library G from Tetraodon nigroviridis, genomic survey
sequence.

ACCESSION AL272948
VERSION AL272948.1 GI:7995193
KEYWORDS GSS: genome survey sequence.
Tetraodon nigroviridis.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis

REFERENCE 1 (bases 1 to 953)
AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bertot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence

TITLE Unpublished
JOURNAL 2 (bases 1 to 953)
REFERENCE Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bertot,A. and
Weissenbach,J.

TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished

```

REFERENCE 3 (bases 1 to 953)
AUTHORS   Genoscope.
TITLE     Direct Submission
JOURNAL   Submitted (12-APR-2000)
COMMENT   This sequence is a single read and was generated as part of a large
          scale clone-end sequencing project of the Tetraodon nigroviridis
          genome. For more information, please take a look at
          http://www.genoscope.cns.fr/tetraodon.
FEATURES
  source
    1..953
      /organism="Tetraodon nigroviridis"
      /db_xref="taxon:99883"
      /clone="079N02"
      /clone_lib="G"
      /note="Genoscope sequence ID : COBG079DG01SP1-end :
        PUC-Ori"
BASE COUNT 316 a 218 c 176 g 238 t 5 others
ORIGIN
Query Match 75.0%; Score 24; DB 17; Length 953;
Best Local Similarity 84.4%; Pred. No. 98;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TAATACACACATATTAATTGTTGTTGTTATTA 32
    ||||| ||| ||||| ||||| ||||| |||||
Db 233 TAATAAACTCAATATTTATTTGGGTTTATTA 202

RESULT 2
AZ523535/c
LOCUS      510 bp DNA linear GSS 07-MAY-2001
DEFINITION 220PbF09 Pb MBN #21 Plasmodium berghei genomic 3', DNA sequence.
ACCESSION  AZ523535
VERSION     AZ523535.1 GI:13962603
KEYWORDS   GSS.
SOURCE     Plasmodium berghei.
ORGANISM   Plasmodium berghei
REFERENCE  1 (bases 1 to 510)
AUTHORS   Carlton,J.M.-R. and Dame,J.B.
TITLE     The Plasmodium vivax and P. berghei gene sequence tag projects
JOURNAL   Parasitol Today (Regul. Ed.) 16 (10), 409 (2000)
COMMENT   Contact: Dame JB
          Dept. of Pathobiology, College of Veterinary Medicine
          University of Florida
          2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA
          Tel: 352 392 4700
          Fax: 352 392 9704
          Email: damejb@mail.vetmed.ufl.edu
          Seq primer: M13(-20) forward
          Class: shotgun.
FEATURES
  source
    1..510
      /organism="Plasmodium berghei"
      /strain="ANKA clone 15cyl (clone of the ANKA 8417 clone)"
      /db_xref="taxon:5821"
      /clone_lib="Pb MBN #21"
      /dev_stage="asexual blood forms"
      /lab_host="Mus musculus"
      /note="Vector: pBluescript SK(+) vector DNA, phagenid
        excised from lambda ZAP; Site_1: EcoRV; Site_2: EcoRV;
        Genomic DNA was prepared from asynchronous blood stage
        forms of the cloned ANKA isolate of P. berghei grown in
        laboratory Swiss white mice. The DNA was purified from
        contaminating host DNA by Hoechst Dye 33258-CsCl
        ultracentrifugation and precipitated. Purified DNA was
        digested with 50 C, as described in the presence of 36-38%
        formamide at 50 C, as described (Vernick, K.D., Imberski,
        R.B., and McCutchan, T.P. 1988. Nucleic Acids Research
        16:6883-6896). The ends of the digestion fragments were
        polished using T4 DNA polymerase, and the fragments size
        selected in the range 500-2000 bp. These were ligated into
        the EcoRV-cleaved and dephosphorylated pBluescript SK(+)
```

```

vector. Recombinant plasmids were used to transform E.
coli XL10-Gold host cells."
BASE COUNT 177 a 65 c 42 g 226 t
ORIGIN
Query Match 73.8%; Score 23.6; DB 17; Length 510;
Best Local Similarity 86.7%; Pred. No. 1.4e+02;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TAATACACACATATTAATTGTTGTTGTTAT 30
    ||||| ||||| ||||| ||||| ||||| |||||
Db 502 TAATAAACAAATAATAATTTGTTTAT 473

RESULT 3
CI9D10/c
LOCUS      700 bp DNA linear GSS 03-DEC-2000
DEFINITION Ciona intestinalis genomic fragment, clone 9D10, genomic survey
          sequence.
ACCESSION  AJ227574
VERSION     AJ227574.1 GI:2951400
KEYWORDS   GSS; genome survey sequence.
SOURCE     Ciona intestinalis.
ORGANISM   Ciona intestinalis
          Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
          Phlebobranchia; Cionidae; Ciona.
REFERENCE  1 (bases 1 to 700)
AUTHORS   Simmen,M.W., Leitgeb,S., Clark,V.H., Jones,S.J. and Bird,A.
TITLE     Gene number in an invertebrate chordate, Ciona intestinalis
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 95 (8), 4437-4440 (1998)
MEDLINE   98208558
PUBMED    9539755
REFERENCE  2 (bases 1 to 700)
AUTHORS   Simmen,M.W., Leitgeb,S., Charlton,J., Jones,S.J., Harris,B.R.,
          Clark,V.H. and Bird,A.
TITLE     Nonmethylated transposable elements and methylated genes in a
          chordate genome
JOURNAL   Science 283 (5405), 1164-1167 (1999)
MEDLINE   99148102
PUBMED    10024242
REFERENCE  3 (bases 1 to 700)
AUTHORS   Simmen,M.W. and Bird,A.
TITLE     Sequence analysis of transposable elements in the sea squirt, Ciona
          intestinalis
JOURNAL   Mol. Biol. Evol. 17 (11), 1685-1694 (2000)
MEDLINE   20523971
PUBMED    11070056
REFERENCE  4 (bases 1 to 700)
AUTHORS   Clark,V.H., Leitgeb,S., Charlton,J., Tweedie,S., Simmen,M.W. and
          Bird,A.P.
TITLE     Direct Submission
JOURNAL   Submitted (28-FEB-1998) ICMB, University of Edinburgh, King's
          Buildings, Mayfield Rd, Edinburgh EH9 3JR, UK. E-mail contact:
          VCIARK@sv0.bio.ed.ac.uk
          Vector: pBluescript KS.
FEATURES
  source
    1..700
      /organism="Ciona intestinalis"
      /db_xref="taxon:7719"
      /clone="9D10"
      /dev_stage="adult"
BASE COUNT 251 a 105 c 115 g 229 t
ORIGIN
Query Match 72.5%; Score 23.2; DB 17; Length 700;
Best Local Similarity 89.3%; Pred. No. 1.9e+02;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 ACAACACAAATTAATTGTTGTTGTTATTA 32
    ||||| ||||| ||||| ||||| ||||| |||||
Db 673 ACAACACAGTATAAATTTGTTGTTATTA 646
```

```

RESULT 4
AA677944/c
LOCUS
DEFINITION
  459 bp mRNA linear EST 19-DEC-1997
  z124h07.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA
  clone IMAGE:431773 3', mRNA sequence.
ACCESSION
AA677944
VERSION
AA677944.1 GI:2658466
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 459)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wyllie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. Et from Amersham
High quality sequence stop: 451.
Location/Qualifiers
1..459
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:431773"
/clone_lib="Soares_fetal_liver_spleen_INFLS_S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site.1: Pac I; Site.2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen INFLS library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer [5'
ACTGCGAGCAATTAATTAAGATCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT
145 a 82 c 102 g 129 t 1 others
ORIGIN
Query Match 71.9%; Score 23; DB 9; Length 459;
Best Local Similarity 83.9%; Pred. No. 2.3e+02;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AATACACACAAATATTAATGTGTTGTTATTA 32
|||||
Db 410 AATATAACACAAATATTAATGTGTTGTTATGA 380

RESULT 5
CNS002SR
LOCUS
DEFINITION
  1101 bp DNA linear GSS 03-JUN-1999
  Drosophila melanogaster genome survey sequence TET3 end of BAC #
  BACR07G08 of RPCT-98 library from Drosophila melanogaster (fruit
  fly), genomic survey sequence.
ACCESSION
AL063320
VERSION
AL063320.1 GI:4941177
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster.
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazuoto Osoegawa and
Aaron Hammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCT-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
1..1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR07G08"
/clone_lib="RPCT-98"
/note="end : TET3"
BASE COUNT
248 a 214 c 174 g 374 t 91 others
ORIGIN
Query Match 71.2%; Score 22.8; DB 17; Length 1101;
Best Local Similarity 65.6%; Pred. No. 2.6e+02;
Matches 21; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 TAATACACACAAATATTAATGTGTTGTTATTA 32
|||||
Db 940 TAATASASASAAAATTAATGTGTTTATTATW 971

RESULT 6
AA101244
LOCUS
DEFINITION
  526 bp mRNA linear EST 28-OCT-1996
  zn43b06.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone
  IMAGE:550163 3', mRNA sequence.
ACCESSION
AA101244
VERSION
AA101244.1 GI:1647884
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 526)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins
,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,
Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham

```

High quality sequence stop: 233.

FEATURES

Location/Qualifiers
1. .526
/organism="Homo sapiens"
/db_xref="GDB:3928681"
/db_xref="taxon:9606"
/clone="IMAGE:550163"
/clone_lib="Stratagene HeLa cell s3 937216"
/sex="female"
/dev_stage="HeLa S3 cell line"
/lab_host="SOLR (kanamycin resistant)"
/note="Vector: pBluescript SK-; Site.1: EcoRI; Site.2: XhoI; Cloned unidirectionally. Primer: Oligo dT. HeLa S3 epitheloid carcinoma cells grown to semi-confluency without induction. Average insert size: 1.5 kb; Uni-ZAP XR Vector. -5' adaptor sequence: 5' GAATTCGGCAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3'"

BASE COUNT 202 a 94 c 57 g 165 t 8 others

ORIGIN

Query Match 70.6%; Score 22.6; DB 9; Length 526;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TAATACACACATATTAATGTGTGTAT 30

||||||| ||||||| ||||||| |||

Db 390 TAATACAGCNAATATTAATGTGTAT 419

RESULT 7

AQ970499 523 bp DNA linear GSS 28-JAN-2000
LOCUS RPCI-23-325C1.TJ RPCI-23 Mus musculus genomic clone RPCI-23-325C1,
DEFINITION DNA sequence.

ACCESSION

VERSION AQ970499

KEYWORDS GSS.

SOURCE AQ970499.1 GI:6800952

house mouse.

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret
B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-23

Unpublished (1999)

Other_GSSs: RPCI-23-325C1.TV

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@jorg.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Plate: 325 row: C column: 1

Seq primer: SP6

Class: BAC ends.

Location/Qualifiers

1. .523

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-23-325C1"

/clone_lib="RPCI-23"

/sex="Female"

/lab_host="DH10B"

FEATURES

source

/note="Organ: Kidney/Brain; Vector: pBACE3.6; Site.1: EcoRI; Site.2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI. Methyase. Size selected DNA was cloned into the pBACE3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 173 a 109 c 120 g 120 t 1 others

ORIGIN

Query Match 70.0%; Score 22.4; DB 17; Length 523;

Best Local Similarity 81.2%; Pred. No. 3.7e+02;

Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TAATACACACATATTAATGTGTGTATTA 32

||||||| ||||||| ||||||| |||

Db 70 TAATACATATATTAATTAATGTGTAGTA 101

RESULT 8

AZ848763/C

LOCUS AZ848763

DEFINITION 2M0149H21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0149H21 R, DNA sequence.

ACCESSION AZ848763

VERSION AZ848763.1

KEYWORDS GSS.

SOURCE AZ848763.1 GI:13032165

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 562)

REFERENCE 1 (bases 1 to 562)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0149 row: H column: 21

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 562.

Location/Qualifiers

1. .562

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0149H21"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/note="Vector: PWB42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN

240 a 80 c 91 g 151 t

Query Match 70.0%; Score 22.4; DB 17; Length 562;
Best Local Similarity 81.2%; Pred. No. 3.7e+02;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TAATAACACACAATTAATGTTGTTGTTATTA 32

Db 265 TAATACCACACAATCTTAATGATTGGTAAATA 234

RESULT 9
LOCUS

DEFINITION BQ692893 584 bp mRNA linear EST 15-JUL-2002
pt08d12.y1 Trichinella spiralis immature L1 pAMP1 v1 Trichinella
spiralis CDNA 5' similar to SW:AQP9_HUMAN O43315 AQUAPORIN 9. ;
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

BQ692893.1 GI:21818209

ORGANISM

Trichinella spiralis.

Eukaryota: Metazoa;

Trichinellidae; Trichinella.

1 (bases 1 to 584)

McCarte,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.,
Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,
Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagarelshvili,R.,
Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn.S.,
Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
Wilson,R.

The Washington Univ. Nematode EST Project, 1999

Unpublished (1999)

Contact: McCarte JP

The Washington Univ. Nematode EST Project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

The library was constructed by Claire Murphy and Dr. James McCarter
at Washington University, St. Louis. Newborn larvae were collected
from infected rats and provided by Dr. Judith Appleton of Cornell
University, Ithaca, NY (jaa2@cornell.edu).

Seq primer: -40RP from Gibco

High quality sequence stop: 415.

FEATURES

Location/Qualifiers

1..584

/organism="Trichinella spiralis"

/db_xref="taxon:6334"

/clone_lib="Trichinella spiralis immature L1 pAMP1 v1"

/dev_stage="immature L1"

/lab_host="DH10B"

/note="Vector: pAMP1 (Gibco); Site_1: NotI; Site_2: SalI;

The library was constructed by Claire Murphy and Dr. James

McCarter at Washington University, St. Louis. The cDNA was

made by using Dynabead oligo-dT priming (Dynal). PCR based

library using a modified protocol from the SMART PCR cDNA

Synthesis Kit from Clontech. Directionally cloned into the

UDG sites of pAMP1. Newborn larvae were collected from the

infected rats and provided by Dr. Judith Appleton of

Cornell University, Ithaca, NY (jaa2@cornell.edu)."

BASE COUNT
ORIGIN

149 a 110 c 139 g 186 t

Query Match 70.0%; Score 22.4; DB 14; Length 584;
Best Local Similarity 81.2%; Pred. No. 3.7e+02;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TAATACACACAATTAATGTTGTTGTTATTA 32

Db 148 TATTATAATATTATTAATGTTGTTGTTATTA 117

RESULT 10
LOCUS

DEFINITION AQ450340 633 bp DNA linear GSS 08-APR-1999
500010F04.x1 CpIOWAM13mp18gDNA1 Cryptosporidium parvum genomic, DNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

AQ450340.1 GI:4579477

ORGANISM

Cryptosporidium parvum.

Cryptosporidium parvum

Eukaryota; Alveolata; Apicomplexa; Coccidia; Elmeriida;

Cryptosporidiidae; Cryptosporidium.

1 (bases 1 to 633)

Hyman,R.W., Fung,E., Qin,F., Rowley,D. and Davis,R.W.

Cryptosporidium parvum genome sequencing demonstration project

Unpublished (1999)

Contact: Hyman, R. W.

Stanford DNA Sequencing and Technology Center

Stanford University School of Medicine, Palo Alto

855 California Avenue, Palo Alto, CA 94304, USA

Tel: 650 812 1972

Fax: 650 812 1975

Email: hyman@sequence.stanford.edu

For Annotation Data see http://medsfgh.ucsf.edu/id/CpTags/home.html

Seq primer: M13(-21) forward

Class: shotgun.

FEATURES

Source

1..633

/organism="Cryptosporidium parvum"

/strain="IOWA"

/db_xref="taxon:5807"

/clone_lib="CpIOWAM13mp18gDNA1"

/lab_host="E. coli DH125"

/note="Vector: M13mp18; Site_1: Hind III; C. parvum (IOWA

isolate) genomic DNA was hydrodynamically sheared to

produce fragments having a tight size distribution between

1.5 and 3 kb. Adaptors (pGTGACTCA/CAAAACCACTGAGTp) were

ligated to the randomly sheared gDNA fragments and

PAGCTGTGTG linkers were ligated to the Hind III-cleaved

M13mp18 vector. The adaptor-containing inserts were

annealed and ligated to the vector and transformed into *E.*

coli strain DH125. Recombinant phagemid clones from the

first plating of the library were randomly selected for

sequence analysis using the M13(-21) forward primer."

BASE COUNT 236 a 77 c 101 g 219 t

ORIGIN

Query Match 70.0%; Score 22.4; DB 17; Length 633;

Best Local Similarity 81.2%; Pred. No. 3.7e+02;

Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TAATACACACAATTAATGTTGTTGTTATTA 32

Db 337 TTATGCACAAACAATTTTAATGGGCTGTATTA 306

RESULT 11
LOCUS

DEFINITION BJ365887 239 bp mRNA linear EST 08-MAR-2002
dictyostelium discoidium cDNA library, Cf Dictyostelium
discoidium cDNA clone ddc36n24 5', mRNA sequence.

ACCESSION

BJ365887

VERSION BJ365887.1 GI:19275189

Thu Feb 13 12:34:57 2003

```

KEYWORDS
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum
REFERENCE Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
AUTHORS 1 (bases 1 to 239)
TITLE Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
JOURNAL Full length cDNA of Dictyostelium discoideum at the culmination
COMMENT stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES
Location/Qualifiers
source
1..239
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="ddc36n24"
/clone_lib="Dictyostelium discoideum cDNA library, CF"
/sex="mat A"
/dev_stage="Culmination stage"
BASE COUNT 113 a 26 c 1 g 99 t
ORIGIN
Query Match 68.8%; Score 22; DB 13; Length 239;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AATAACACACAATAATTAATGTGTGTTATT 31
|||||
DB 92 AATAACACACAATAATTAATTTTCTT 121

RESULT 12
AV385246 505 bp mRNA linear EST 27-OCT-1999
LOCUS AV385246 Halocynthia roretzi Fertilized egg Halocynthia roretzi
DEFINITION cDNA clone 005A08_3 3', mRNA sequence.
ACCESSION AV385246
VERSION AV385246.1 GI:6130303
KEYWORDS EST.
SOURCE Halocynthia roretzi.
ORGANISM Halocynthia roretzi
REFERENCE Makabe,K.W.
AUTHORS Halocynthia roretzi
TITLE Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
JOURNAL Stolidobranchia; Pyuridae; Halocynthia.
COMMENT 1 (bases 1 to 505)
Makabe,K.W.
Kyoto University
Department of Zoology, Graduate School of Science
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4095
Fax: 81-75-705-1113
Email: kwmakabe@sci.kyoto-u.ac.jp.
FEATURES
Location/Qualifiers
source
1..505
/organism="Halocynthia roretzi"
/db_xref="taxon:7729"
/clone="005A08_3"
/clone_lib="Halocynthia roretzi Fertilized egg"
/dev_stage="Fertilized egg"
/note="Organ: embryo"
BASE COUNT 175 a 79 c 65 g 186 t
ORIGIN
Query Match 68.8%; Score 22; DB 10; Length 505;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;

QY 3 ATACACACAATAATTAATGTGTGTTATTA 32
|||||
DB 313 ATTCAACAGATATTAATTTTATTA 342

RESULT 14
CNS05J05 1042 bp DNA linear GSS 26-MAY-2000
LOCUS CNS05J05/c Tetraodon nigroviridis genome survey sequence SP6 end of clone
DEFINITION 017F15 of library B from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL340430
VERSION AL340430.1 GI:8234188
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.

```

```

Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TAATACACACAATAATTAATGTGTGTTAT 30
|||||
DB 299 TCAACATAACAATAATTAATGTGTATAT 328

RESULT 13
AQ319355 571 bp DNA linear GSS 06-MAY-1999
LOCUS RPC111-97J9.TJ RPC1-11 Homo sapiens genomic clone RPC1-11-97J9, DNA
DEFINITION sequence.
ACCESSION AQ319355
VERSION AQ319355.1 GI:4052320
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 571)
Adams M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
Unpublished (1998)
Other_GSSs: RPC111-97J9.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPC1-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
FEATURES
Location/Qualifiers
source
1..571
/organism="Homo sapiens"
/db_xref="GDB:7537088"
/db_xref="taxon:9606"
/clone="RPC1-11-97J9"
/clone_lib="RPC1-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC111 Human Male BAC Library"
BASE COUNT 197 a 88 c 100 g 186 t
ORIGIN
Query Match 68.8%; Score 22; DB 17; Length 571;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 ATACACACAATAATTAATGTGTGTTATTA 32
|||||
DB 313 ATTCAACAGATATTAATTTTATTA 342

RESULT 14
CNS05J05 1042 bp DNA linear GSS 26-MAY-2000
LOCUS CNS05J05/c Tetraodon nigroviridis genome survey sequence SP6 end of clone
DEFINITION 017F15 of library B from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL340430
VERSION AL340430.1 GI:8234188
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.

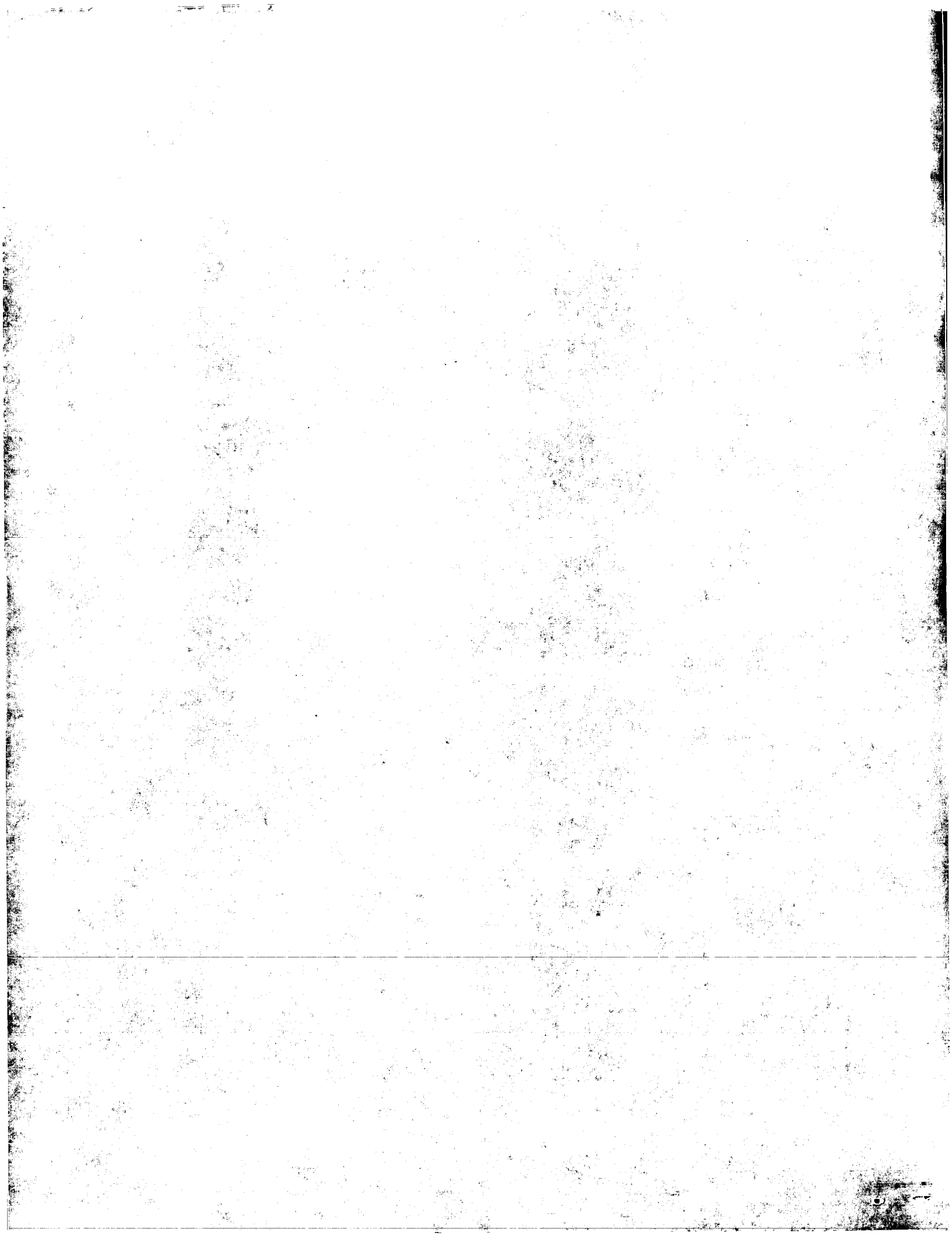
```

ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
REFERENCE 1 (bases 1 to 1042)
AUTHORS Roest-Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
TITLE Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1042)
AUTHORS Roest-Crolius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1042)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000)
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
Location/Qualifiers
1..1042
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="017F15"
/clone_lib="B"
BASE COUNT 297 a 213 c 219 g 282 t 31 others
ORIGIN
Query Match 68.1%; Score 21.8; DB 17; Length 1042;
Best Local Similarity 92.0%; Pred. No. 5.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 7 AACACAAATTAATTGTGTGTATT 31
||||| ||||| ||||| ||||| |||||
Db 71 AACACAAATTAATTGTGTGTATT 47
RESULT 15
B0693146
LOCUS
DEFINITION B0693146 536 bp mRNA linear EST 15-JUL-2002
ptile07.y1 Trichinella spiralis immature L1 pAMP1 v1 Trichinella
spiralis cDNA 5' similar to SW:EFIA_ONCVO P27592 ELONGATION FACTOR
1-ALPHA ; , mRNA sequence.
ACCESSION B0693146
VERSION B0693146.1 GI:21818462
KEYWORDS EST.
SOURCE Trichinella spiralis.
ORGANISM Trichinella spiralis
Eukaryota; Metazoa; Nematoda; Enoplea; Trichocephalida;
Trichinellidae; Trichinella.
REFERENCE 1 (bases 1 to 536)
AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.,
Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,
Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagarishvili,R.,
Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
Wilson,R.
TITLE The Washington Univ. Nematode EST Project, 1999
JOURNAL Unpublished (1999)
COMMENT Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800
Fax: 314 286 1810
Email: estevatson.wustl.edu
The library was constructed by Claire Murphy and Dr. James McCarter
at Washington University, St. Louis. Newborn larvae were collected
from infected rats and provided by Dr. Judith Appleton of Cornell
University, Ithaca, NY (jaa2@cornell.edu).
Seq primer: -40RP from Gibco
High quality sequence stop: 414.
Location/Qualifiers
1..536
/organism="Trichinella spiralis"
/db_xref="taxon:6334"
/clone_lib="Trichinella spiralis immature L1 pAMP1 v1"
/dev_stage="Immature L1"
/lab_host="DHI0B"
/note="Vector: pAMP1 (Gibco); Site 1: NotI; Site 2: SalI;
The library was constructed by Claire Murphy and Dr. James
McCarter at Washington University, St. Louis. The cDNA was
made by using Dynabead oligo-dr priming (Dyna). PCR based
library using a modified protocol from the SMART PCR cDNA
Synthesis Kit from Clontech. Directionally cloned into the
UDG sites of pAMP1. Newborn larvae were collected from
infected rats and provided by Dr. Judith Appleton of
Cornell University, Ithaca, NY (jaa2@cornell.edu)."
BASE COUNT 171 a 85 c 110 g 170 t
ORIGIN

Query Match 67.5%; Score 21.6; DB 14; Length 536;
Best Local Similarity 85.7%; Pred. No. 7.2e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 TACACACAAATTAATTGTGTGTATT 31
||||| ||||| ||||| ||||| |||||
Db 411 TATAGGCAATTAATTGTGTATT 438
Search completed: February 13, 2003, 03:17:52
Job time : 2259 secs

FEATURES
source



GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 13, 2003, 01:45:51 ; Search time 298 Seconds
(without alignments)
1881.703 Million cell updates/sec

Title: US-09-895-435-4
Perfect score: 249
Sequence: 1 ggggtaccgcagcatttcg.....gacgcggaggaaatcatcg 249

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_101002.*

1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	38	15.3	5216	20 AAX07548	PKS90 TIR coupling
C 2	38	15.3	5230	20 AAX07549	PTREX1 mutant beta
C 3	38	15.3	5230	21 AAA15041	Nucleotide sequenc
C 4	38	15.3	5231	20 AAX07550	PTREX1A mutant bet
C 5	38	15.3	5497	22 AAF29646	Plasmid pTlmpTFL
C 6	38	15.3	5770	21 AAA15043	Nucleotide sequenc
C 7	38	15.3	5870	21 AAA15044	Nucleotide sequenc
C 8	38	15.3	5906	21 AAA15042	Nucleotide sequenc
C 9	19	7.6	1566	20 AAX13472	Enterococcus faeca

C 10	19	7.6	6076	22 AAS46664	Tumour suppressor
C 11	19	7.6	6136	24 ABK40042	Human chemically p
C 12	19	7.6	7008	22 AAS46531	Tumour suppressor
C 13	19	7.6	140036	24 AAS98600	Human genomic DNA
C 14	18	7.2	251	21 AAC22654	Human secreted pro
C 15	18	7.2	286	24 ABN16703	Human ORFX polynuc
C 16	18	7.2	342	22 AAH69737	Human cervical can
C 17	18	7.2	345	22 AAH73166	Human cervical can
C 18	18	7.2	457	22 ABA44883	Human foetal cell
C 19	18	7.2	457	22 ABA53346	Human foetal liver
C 20	18	7.2	457	22 ABA25077	Probe #3543 for ge
C 21	18	7.2	457	22 AAK03588	Human brain expres
C 22	18	7.2	457	22 AAK29048	Human bone marrow
C 23	18	7.2	457	22 AAI13636	Probe #3569 for ge
C 24	18	7.2	457	22 AAI34995	Probe #3681 used t
C 25	18	7.2	457	22 AAI03520	Probe #3511 used t
C 26	18	7.2	457	24 ABS03593	Human genome-deriv
C 27	18	7.2	474	16 AAT19891	Human gene signatu
C 28	18	7.2	514	22 AAH70477	Human cervical can
C 29	18	7.2	557	22 ABL11160	Human cDNA clone (
C 30	18	7.2	602	23 ABL13041	Drosophila melanog
C 31	18	7.2	913	22 AAL23181	Human breast cance
C 32	18	7.2	1213	24 ABL55491	Alpha-catenin 10.3
C 33	18	7.2	2246	24 ABK54129	cDNA encoding huma
C 34	18	7.2	2561	23 ABL02994	Drosophila melanog
C 35	18	7.2	2582	23 ABL24840	Drosophila melanog
C 36	18	7.2	2642	22 AAH17727	Human cDNA sequenc
C 37	18	7.2	2673	21 AAC76657	Human ORFX ORF2212
C 38	18	7.2	2695	23 ABL27234	Drosophila melanog
C 39	18	7.2	2717	23 ABL13040	Drosophila melanog
C 40	18	7.2	2733	22 AAH33639	Human colon cancer
C 41	18	7.2	2947	22 AAH44832	Rat cDNA encoding
C 42	18	7.2	3181	22 ABA08899	Human secreted pro
C 43	18	7.2	4704	22 AAL36927	Human musculoskele
C 44	18	7.2	4704	22 AAK67840	Human immune/haema
C 45	18	7.2	4704	22 AAK73415	Human immune/haema

ALIGNMENTS

RESULT 1
AAX07548/C
ID AAX07548 standard; DNA; 5216 BP.
XX
AC AAX07548;
XX
08-JUN-1999 (first entry)
DT
DE PKS90 TIR coupling vector.
XX
KW Beta-toxin; cpb; vaccine; infection; protection;
KW retained immunogenicity; haemorrhagic enteritis; necrotic enteritis;
KW enterotoxemia; lamb dysentery; translation initiation region; ds.
XX Synthetic.
OS
XX EP892054-AL.
PN
PD 20-JAN-1999.
XX
PF 17-JUN-1998; 98EP-0202032.
XX
PR 20-JUN-1997; 97EP-0201888.
XX (ALKU) AKZO NOBEL NV.
XX
PI Frandsen PL, Sengers RPAM, Waterfield NR, Wells JM;
XX WPI; 1999-083571/08.
XX
PT New detoxified derivative of Clostridium perfringens beta-toxin -
PT with retained immunogenicity, useful as a vaccine to protect against

PT Clostridium perfringens infection
 PS Example; Fig 2b; 30pp; English.
 XX
 XX The sequence is that of the vector pKS90 which was used in the
 CC construction of a detoxified immunogenic derivative of Clostridium
 CC perfringens beta-toxin. Such a derivative is useful as a vaccine
 CC to induce an immune response and protect against Clostridium
 CC perfringens infection in man, pig, lamb, sheep, goat, calf and
 CC bird, which causes haemorrhagic enteritis, necrotic enteritis,
 CC enterotoxemia and lamb dysentery. The new beta-toxin has been
 CC detoxified without impairing the immunogenicity, unlike prior
 CC art vaccines which used chemical and formalin detoxifying methods.
 CC Production of the beta-toxin in gram positive bacteria prevents
 CC prior art difficulties of isolation from dangerous Clostridium
 CC perfringens, and purification from the Clostridium perfringens spores.
 XX
 SQ Sequence 5216 BP; 1934 A; 790 C; 980 G; 1512 T; 0 other;
 Query Match 15.3%; Score 38; DB 20; Length 5216;
 Best Local Similarity 100.0%; Pred. No. 2.9e-08;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGGTACCGCCAGCATTTCCGAAAAAACCACGCTAAG 38
 DB 2309 GGGGTACCGCCAGCATTTCCGAAAAAACCACGCTAAG 2272
 RESULT 2
 AAX07549/c
 ID AAX07549 standard; DNA; 5230 BP.
 AC AAX07549;
 XX
 XX 08-JUN-1999 (first entry)
 DT
 DE pTREX1 mutant beta-toxin expression cassette.
 XX
 XX Beta-toxin; cpb; vaccine; infection; protection;
 KW retained immunogenicity; haemorrhagic enteritis; necrotic enteritis;
 KW enterotoxemia; lamb dysentery; ds.
 XX
 OS Synthetic.
 XX
 XX EP892054-A1.
 PN
 XX 20-JAN-1999.
 PD
 XX 17-JUN-1998; 98EP-0202032.
 PF
 XX 20-JUN-1997; 97EP-0201888.
 PR
 XX (ALKU) AKZO NOBEL NV.
 PA
 XX Frandsen PL, Sergers RPAW, Waterfield NR, Wells JM;
 PI WPI; 1999-083571/08.
 DR
 XX New detoxified derivative of Clostridium perfringens beta-toxin -
 PT with retained immunogenicity, useful as a vaccine to protect against
 PT Clostridium perfringens infection
 PT
 XX Example; Fig 1c; 30pp; English.
 PS
 XX The sequence is that of the pTREX1 expression cassette which was used in
 CC the construction of a detoxified immunogenic derivative of Clostridium
 CC perfringens beta-toxin. Such a derivative is useful as a vaccine
 CC to induce an immune response and protect against Clostridium
 CC perfringens infection in man, pig, lamb, sheep, goat, calf and
 CC bird, which causes haemorrhagic enteritis, necrotic enteritis,
 CC enterotoxemia and lamb dysentery. The new beta-toxin has been
 CC detoxified without impairing the immunogenicity, unlike prior
 CC art vaccines which used chemical and formalin detoxifying methods.

CC Production of the beta-toxin in gram positive bacteria prevents
 CC prior art difficulties of isolation from dangerous Clostridium
 CC perfringens, and purification from the Clostridium perfringens spores.
 XX
 SQ Sequence 5230 BP; 1930 A; 795 C; 983 G; 1522 T; 0 other;
 Query Match 15.3%; Score 38; DB 20; Length 5230;
 Best Local Similarity 100.0%; Pred. No. 2.9e-08;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGGTACCGCCAGCATTTCCGAAAAAACCACGCTAAG 38
 DB 2323 GGGGTACCGCCAGCATTTCCGAAAAAACCACGCTAAG 2286
 RESULT 3
 AAA15041/c
 ID AAA15041 standard; DNA; 5230 BP.
 XX
 AC AAA15041;
 XX
 XX 21-AUG-2000 (first entry)
 DT
 DE Nucleotide sequence of expression plasmid pTREX1.
 XX
 XX Intestinal mucosa; cytokine; cytokine antagonist; anti-inflammatory;
 KW Gram-positive bacteria; Lactococcus lactis; gastrointestinal tract;
 KW inflammatory bowel disease; chronic colitis; Crohn's disease; IL10;
 KW ulcerative colitis; tumour necrosis factor; TNF; interleukin 10; ss.
 XX
 OS Synthetic.
 XX
 XX WO200023471-A2.
 PN
 XX 27-APR-2000.
 PD
 XX 06-OCT-1999; 99WO-EP07800.
 PF
 XX 20-OCT-1998; 98EP-0203529.
 PR
 XX (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
 PA
 XX Steidler L, Remaut ER, Fiers W;
 PI WPI; 2000-422481/36.
 DR
 XX Treating inflammatory bowel diseases comprises administering a
 PT composition comprising a cytokine-producing or cytokine
 PT antagonist-producing Gram-positive bacterial strain -
 PT
 XX Disclosure; Fig 1B; 45pp; English.
 PS
 XX The present sequence represents an expression plasmid for use in the
 CC course of the invention. The specification describes an administration
 CC strategy for the delivery at the intestinal mucosa of cytokines or
 CC cytokine antagonists, preferably of acid sensitive anti-inflammatory
 CC agents such as interleukin 10 (IL10) or tumour necrosis factor (TNF).
 CC The method uses a cytokine-producing or cytokine antagonist-producing
 CC Gram-positive bacterial strain (such as Lactococcus lactis). The use of
 CC non-colonizing bacteria expressing cytokines or cytokine antagonists
 CC allows the treatment to be directed to the disease site, whilst
 CC minimizing the possibility of degradation along the gastrointestinal
 CC tract. The recombinant bacteria are used in the treatment of inflammatory
 CC bowel diseases, especially chronic colitis, Crohn's disease or an
 CC ulcerative colitis.
 XX
 SQ Sequence 5230 BP; 1930 A; 796 C; 982 G; 1522 T; 0 other;
 QY
 XX Query Match 15.3%; Score 38; DB 21; Length 5230;
 Best Local Similarity 100.0%; Pred. No. 2.9e-08;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGGTACCGCCAGCATTTCCGAAAAAACCACGCTAAG 38

```

Db 2323 GGGGTACCGCCAGCATTTTCGGAAAAAACCCAGCGCTAAG 2286
|||||
RESULT 4
AAAX07550/c
ID AAX07550 standard; DNA: 5231 BP.
XX
AC AAX07550;
XX
DT 08-JUN-1999 (first entry)
XX
DE pTREX1A mutant beta-toxin expression cassette.
XX
KW Beta-toxin; cpb; vaccine; infection; protection;
KW retained immunogenicity; haemorrhagic enteritis; necrotic enteritis;
KW enterotoxemia; lamb dysentery; ds.
XX
OS Synthetic.
XX
PN EP892054-Al.
XX
PD 20-JAN-1999.
XX
PF 17-JUN-1998; 98EP-0202032.
XX
PR 20-JUN-1997; 97EP-0201888.
XX
PA (ALKU ) AKZO NOBEL NV.
XX
PI Frandsen PL, Sergers RPAM, Waterfield NR, Wells JM;
XX
DR WPT; 1999-083571/08.
XX
PT New detoxified derivative of Clostridium perfringens beta-toxin -
PT with retained immunogenicity, useful as a vaccine to protect against
PT Clostridium perfringens infection
XX
PS Example; Fig 1b; 30pp; English.
XX
CC The sequence is that of the pTREX1A expression cassette which was used
CC in the construction of a detoxified immunogenic derivative of Clostridium
CC perfringens beta-toxin. Such a derivative is useful as a vaccine
CC to induce an immune response and protect against Clostridium
CC perfringens infection in man, pig, lamb, sheep, goat, calf and
CC bird, which causes haemorrhagic enteritis, necrotic enteritis,
CC enterotoxemia and lamb dysentery. The new beta-toxin has been
CC detoxified without impairing the immunogenicity, unlike prior
CC art vaccines which used chemical and formalin detoxifying methods.
CC Production of the beta-toxin in gram positive bacteria prevents
CC prior art difficulties of isolation from dangerous Clostridium
CC perfringens, and purification from the Clostridium perfringens spores.
XX
SQ Sequence 5231 BP; 1930 A; 793 C; 985 G; 1523 T; 0 other;

Query Match 15.3%; Score 38; DB 20; Length 5231;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTACCGCCAGCATTTTCGGAAAAAACCCAGCGCTAAG 38
|||||
Db 2324 GGGGTACCGCCAGCATTTTCGGAAAAAACCCAGCGCTAAG 2287
|||||
RESULT 5
AAF29646/c
ID AAF29646 standard; DNA: 5497 BP.
XX
AC AAF29646;
XX
DT 10-APR-2001 (first entry)
XX
DE Plasmid pTlmtTFF1.

```

```

XX Mouse TFF1; mTFF: trefoil protein; antiinflammatory; gastrointestinal;
XX anti-ulcer; peptide therapy; gastrointestinal disease; acute colitis;
XX Crohn's disease; ulcerative colitis; plasmid pTlmtTFF1;
XX recombinant vector; ds.
XX OS Synthetic.
XX PN WO200102570-Al.
XX PD 11-JAN-2001.
XX PF 05-JUL-2000; 2000WO-EP06343.
XX PR 05-JUL-1999; 99EP-0870143.
XX PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX PI Hans WC, Steidler L, Remaut ER;
XX DR WPI; 2001-138142/14.
XX PT Recombinant Lactococcus lactis for delivering a trefoil peptide useful
XX for treating acute or chronic gastrointestinal inflammatory diseases or
XX disorders, e.g. acute or ulcerative colitis, acute flare-ups of Crohn's
XX disease -
XX PS Claim 18; Fig 1c; 44pp; English.
XX
CC The present sequence is a recombinant vector which may be used to
CC generate a recombinant Lactococcus lactis capable of delivering a trefoil
CC peptide in vivo. The recombinant microorganism is useful for
CC manufacturing an agent for the delivery of a trefoil peptide to the
CC gastrointestinal tract, and for treating gastric or intestinal diseases
CC or disorders, or lesions caused by gastric or intestinal diseases or
CC disorders. The microorganism may also be used for preparing medicament to
CC be used for treating gastric and/or gastrointestinal diseases or
CC disorders, acute gastrointestinal inflammatory diseases (e.g., acute
CC colitis, acute flare-ups of Crohn's diseases, or ulcerative colitis), and
CC chronic and spontaneously recurring diseases of the gastrointestinal
CC tract comprising Crohn's disease (enteritis regionalis) and ulcerative
CC colitis (colitis ulcerosa). Disease states which can be treated by the
CC method or compositions comprising the recombinant microorganism or
CC trefoil peptides include disorders of and damage to the alimentary canal,
CC including the mouth, oesophagus, stomach and large and small intestine,
CC as well as for the protection and treatment of tissues that lie outside
CC the alimentary canal.
XX
SQ Sequence 5497 BP; 1994 A; 870 C; 1051 G; 1582 T; 0 other;

Query Match 15.3%; Score 38; DB 22; Length 5497;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTACCGCCAGCATTTTCGGAAAAAACCCAGCGCTAAG 38
|||||
Db 2590 GGGGTACCGCCAGCATTTTCGGAAAAAACCCAGCGCTAAG 2553
|||||
RESULT 6
AAAL5043/c
ID AAAL5043 standard; DNA: 5770 BP.
XX
AC AAAL5043;
XX
DT 21-AUG-2000 (first entry)
XX
DE Nucleotide sequence of expression plasmid pTlmtTFF1.
XX
KW Intestinal mucosa; cytokine; cytokine antagonist; anti-inflammatory;
KW Gram-positive bacteria; Lactococcus lactis; gastrointestinal tract;
KW inflammatory bowel disease; chronic colitis; Crohn's disease; IL10;
KW ulcerative colitis; tumour necrosis factor; TNF; interleukin 10; ss.

```


The present sequence represents an expression plasmid for use in the course of the invention. The specification describes an administration strategy for the delivery at the intestinal mucosa of cytokines or cytokine antagonists, preferably of acid sensitive anti-inflammatory agents such as interleukin 10 (IL10) or tumour necrosis factor (TNF). The method uses a cytokine-producing or cytokine antagonist-producing Gram-positive bacterial strain (such as *Lactococcus lactis*). The use of non-colonizing bacteria expressing cytokines or cytokine antagonists allows the treatment to be directed to the disease site, whilst minimizing the possibility of degradation along the gastrointestinal tract. The recombinant bacteria are used in the treatment of inflammatory bowel diseases, especially chronic colitis, Crohn's disease or an ulcerative colitis.

Query Match 15.3%; Score 38; DB 21; Length 5906;
 Best Local Similarity 100.0%; Pred. No. 2.9e-08;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTACCGCCAGCATTTTCGAAAAAACCACGCTAG 38
 Db 2999 GGGTACCGCCAGCATTTTCGAAAAAACCACGCTAG 2962

RESULT 9
 AAX13472
 ID AAX13472 standard; DNA; 1566 BP.
 AC AAX13472;
 XX
 DT 19-MAR-1999 (first entry)
 XX
 DE Enterococcus faecalis genome contig SEQ ID NO:535.
 XX
 KW Enterococcus faecalis; contig; detection; Enterococcal infection;
 KW vaccine; attenuation; computer readable medium; ds.
 XX
 OS Enterococcus faecalis.
 XX
 PN WO9850555-A2.
 XX
 PD 12-NOV-1998.
 XX
 PE 04-MAY-1998; 98WO-US08985.
 PR 14-NOV-1997; 97US-0066009.
 PR 06-MAY-1997; 97US-0044031.
 PR 16-MAY-1997; 97US-0046655.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Barash SC, Dillion PJ, Kunsch CA;
 XX
 DR WPI; 1999-045171/04.
 XX
 PT New isolated Enterococcus faecalis polynucleotides and polypeptides
 PT - used to develop products for the detection of Enterococcus and for
 PT use in vaccines for prevention or attenuation of Enterococcus
 PT infection.
 XX
 PS Claim 1; Page 1787-1788; 2084pp; English.
 XX
 CC A computer readable medium has been developed which has recorded on it
 CC 982 nucleotide sequences isolated from the Enterococcus faecalis genome.
 CC AAX12938 to AAX13919 represent these nucleotide sequences which are
 CC primary nucleotide sequences, also known as Contigs. The computer-based
 CC system can identify fragments of the Enterococcus faecalis genome with
 CC commercial importance. The products can be used to detect the presence
 CC of Enterococcus faecalis in samples. They can also be used for
 CC diagnosing Enterococcal infection in an animal and monitoring
 CC progression of disease, and for identifying agents which can be used to

CC modulate the growth or pathogenicity of Enterococcus faecalis, or
 CC another related organism, in vivo or in vitro. In particular the
 CC polypeptides encoded by the Enterococcus faecalis nucleotide sequences
 CC can be used in vaccines to prevent or attenuate an Enterococcal
 CC infection.
 XX
 SQ Sequence 1566 BP; 460 A; 273 C; 260 G; 559 T; 14 other;
 Query Match 7.6%; Score 19; DB 20; Length 1566;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 TTTTATACAAAAATAAT 116
 Db 1489 TTTTATACAAAAATAAT 1507

RESULT 10
 AAS46664/c
 ID AAS46664 standard; DNA; 6076 BP.
 XX
 AC AAS46664;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Tumour suppressor gene derived chemically modified sequence #386.
 XX
 KW Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
 KW cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
 KW cytosine methylation; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200168912-A2.
 XX
 PD 20-SEP-2001.
 XX
 PE 15-MAR-2001; 2001WO-EP02955.
 XX
 PR 15-MAR-2000; 2000DE-1013847.
 PR 06-APR-2000; 2000DE-1019058.
 PR 07-APR-2000; 2000DE-1019173.
 PR 30-JUN-2000; 2000DE-1032529.
 PR 01-SEP-2000; 2000DE-1043826.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-602752/68.
 XX
 PT Fragments of chemically modified genes associated with tumour suppressor
 PT genes and oncogenes, useful in designing primers and probes for
 PT analysing diseases associated with cytosine methylation state e.g.
 PT cancer -
 XX
 PS Claim 1; SEQ ID NO 386; 27pp; English.
 XX
 CC The invention relates to a nucleic acid comprising a sequence of 18
 CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
 CC bisulphite, of genes associated with tumour suppression and
 CC oncogenes having a sequence taken from 536 (actually 533 since
 CC numbers 408, 458 and 500 are missing from the sequence listing) sequences
 CC (SS) and sequences complementary to (ss). The nucleic acid may be a
 CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may
 CC form part of a set of probes for detecting the cytosine methylation state
 CC and/or single nucleotide polymorphisms and also to be used in an
 CC array for analysing diseases associated with CpG dinucleotides e.g.
 CC cancers and tumours. The probes can also be used in a method for
 CC ascertaining genetic and/or epigenetic parameters for the diagnosis
 CC and/or therapy of existing diseases or the predisposition to specific
 CC diseases, by analysing cytosine methylations. The parameters may be
 CC compared to another set of genetic and/or epigenetic parameters, the

Thu Feb 13 12:35:00 2003

```
CC differences serving as basis for diagnosis and/or prognosis events which
CC are disadvantageous to patients. The present sequence is one of the
CC 533 genomic sequences derived from tumour suppressor genes and
CC oncogenes. Sequences with even numbered Seq ID numbers are the
CC complementary sequence of the corresponding odd numbered sequence (e.g.
CC ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence
CC is missing).
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 6076 BP; 2013 A; 73 C; 1223 G; 2767 T; 0 other;

Query Match 7.6%; Score 19; DB 22; Length 6076;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 AAAATAATACACACAATA 127
Db 3018 AAAATAATACACACAATA 3000
|||||
|||||

RESULT 11
ABK40042/c
ID ABK40042 standard; DNA; 6136 BP.
XX
AC ABK40042;
XX
XX 21-MAY-2002 (first entry)
XX
XX Human chemically pretreated gene sequence #62 strand 2.
XX
XX Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour;
XX KW Cytostatic; ALDH6; CYP11A; CYP11B1; CYP3A3; DPYD; EPHX2; OCLN; TXNRD1;
XX KW UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.
XX
XX Homo sapiens.
XX
XX WO200202806-A2.
XX
XX 10-JAN-2002.
XX
XX 29-JUN-2001; 2001WO-EP07470.
XX
XX 30-JUN-2000; 2000DE-1032529.
XX PR 01-SEP-2000; 2000DE-1043826.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPT; 2002-154757/20.
XX
XX New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers,
XX useful for detecting cytosine methylation state of genes associated
XX with pharmacogenomics and for therapy of diseases e.g. cancer .
XX
XX Claim 1; SEQ ID No 124; 24pp; English.
XX
XX The invention relates to a nucleic acid comprising a sequence at
XX least 18 bases in length of a segment of the chemically pretreated DNA
XX of genes associated with pharmacogenomics according to one of the
XX sequences of the genes ALDH6 (NM_000693), CYP11A (NM_000781), CYP11B1
XX (NM_000497), CYP3A3 (NM_000776 and NM_017460), DPYD (NM_000110), EPHX2
XX (NM_001979), OCLN (NM_002538), TXNRD1 (NM_003330), UGT8 (NM_003360),
XX MRP (NM_004996), and their complementary sequences, or a sequence (S1) chosen
XX from 87 sequences and their complements. The chemical pretreatment
XX is bisulphite treatment to convert cytosines (but not methyl-cytosines)
XX into uracils. Also included are an oligomer (II) in particular an
XX oligonucleotide or a peptide nucleic acid (PNA)-oligomer, comprising in
XX each case at least one base sequence having a length of 9 nucleotides
XX

CC which hybridises to or is identical to a chemically pretreated DNA of
CC genes associated with pharmacogenomics and their complements, arranged in
CC an array for analysing diseases associated with the methylation state
CC (CpG) and/or detecting SNPs (single nucleotide polymorphisms)
CC of the 87 sequences. The oligomers may also be used as PCR primers.
CC The set of 87 nucleic acids and their complements is useful for diagnosis
CC and therapy of solid tumours and cancer. The present sequence
CC represents one the 87 DNA sequences or its complement.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 6136 BP; 1775 A; 69 C; 1285 G; 3007 T; 0 other;

Query Match 7.6%; Score 19; DB 24; Length 6136;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 ATACAAAAAATAATACAAAC 121
Db 530 ATACAAAAAATAATACAAAC 512
|||||
|||||

RESULT 12
AAS46531
ID AAS46531 standard; DNA; 7008 BP.
XX
AC AAS46531;
XX
XX 18-DEC-2001 (first entry)
XX
XX Tumour suppressor gene derived chemically modified sequence #253.
XX
XX Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
XX KW cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
XX KW cytosine methylation; ds.
XX
XX Homo sapiens.
XX
XX WO200168912-A2.
XX
XX 20-SEP-2001.
XX
XX 15-MAR-2001; 2001WO-EP02955.
XX
XX 15-MAR-2000; 2000DE-1013847.
XX PR 06-APR-2000; 2000DE-1019058.
XX PR 07-APR-2000; 2000DE-1019173.
XX PR 30-JUN-2000; 2000DE-1032529.
XX PR 01-SEP-2000; 2000DE-1043826.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-602752/68.
XX
XX Fragments of chemically modified genes associated with tumour suppressor
XX genes and oncogenes, useful in designing primers and probes for
XX analysing diseases associated with cytosine methylation state e.g.
XX cancer .
XX
XX Claim 1; SEQ ID No 253; 27pp; English.
XX
XX The invention relates to a nucleic acid comprising a sequence of 18
XX bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
XX bisulphite, of genes associated with tumour suppression and
XX oncogenes having a sequence taken from 536 (actually 533 since
XX numbers 408, 458 and 500 are missing from the sequence listing) sequences
XX (Ss) and sequences complementary to (Ss). The nucleic acid may be a
XX peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may
XX form part of a set of probes for detecting the cytosine methylation state
XX
```

CC and/or single nucleotide polymorphisms and also to be used in an
 CC array for analysing diseases associated with CpG dinucleotides e.g.
 CC cancers and tumours. The probes can also be used in a method for
 CC ascertaining genetic and/or epigenetic parameters for the diagnosis
 CC and/or therapy of existing diseases or the predisposition to specific
 CC diseases, by analysing cytosine methylations. The parameters may be
 CC compared to another set of genetic and/or epigenetic parameters, the
 CC differences serving as basis for diagnosis and/or prognosis events which
 CC are disadvantageous to patients. The present sequence is one of the
 CC 533 genomic sequences derived from tumour suppressor genes and
 CC oncogenes.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 7008 BP; 2322 A; 26 C; 1306 G; 3354 T; 0 Other;
 Query Match 7.6%; Score 19; DB 22; Length 7008;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 142 TTAGTGCTTATAATAATA 160
 |||||
 Db 2443 TTAGTGCTTATAATAATA 2461

RESULT 13
 AAS98600/C
 ID AAS98600 standard; DNA; 140036 BP.

AC AAS98600;

DT 12-MAR-2002 (first entry)

DE Human genomic DNA for PHIP/NDRP.

XX PHIP: Pleckstrin homology domain-interacting protein; NDRP; ds;
 KW neuronal differentiation-related protein; insulin receptor substrate;
 KW IRS; signal transducer and activator of transcription; STAT;
 KW transgenic animal; diabetes mellitus type 2; hyperglycaemia;
 KW myotonic muscular dystrophy; acanthosis; nigricans; retinopathy;
 KW nephropathy; arteriosclerosis; peripheral arterial disease; cancer;
 KW adenocarcinoma; leukaemia; breast cancer; prostate cancer; colon cancer;
 KW ovarian cancer; autoimmune disease; inflammation; immunodeficiency.

XX Homo sapiens.

XX WO200185785-A2.

XX 15-NOV-2001.

PF 10-MAY-2001; 2001WO-CA00673.

XX 11-MAY-2000; 2000US-203561P.

PA (ROZA/) ROZAKIS-ADCOCK M.

PA (FARH/) FARHANG-FALLAH J.

PA (CHEN/) CHENG A.

PI Rozakis-Adcock M, Farhang-Fallah J, Cheng A;

XX WPI; 2002-041586/05.

XX Novel Pleckstrin homology domain interacting protein recruiting
 PT proteins of insulin receptor substrate family, and signal transducer
 PT and activator of transcription factors to their receptors, useful to
 PT treat diabetes

PS Disclosure; Page 99-133; 139pp; English.

XX The invention relates to an isolated pleckstrin homology domain
 CC interacting protein (PHIP) that recruits proteins of the insulin

CC receptor substrate (IRS) family, and signal transducer and activator of
 CC transcription (STAT) transcription factors, to receptors that interact
 CC with and phosphorylate the proteins and STAT transcription factors,
 CC the nucleic acid encoding PHIP (nPHIP), a nucleic acid which binds to
 CC nPHIP or regions of it, analogues, fragments or allelic variants of PHIP
 CC or nPHIP, a nucleic acid sequence having substantial sequence identity or
 CC sequence similarity with a nucleic acid sequence fully defined
 CC human neuronal differentiation-related protein (NDRP) nucleic acid
 CC sequence or its exons as given in the specification, expression
 CC vectors and host cells expressing the nucleic acids, anti-PHP antibodies,
 CC and a transgenic animal not already expressing PHIP. The nucleic
 CC acids, proteins and antibodies are useful for diagnosis and treatment of
 CC a condition associated with an insulin receptor (e.g. diabetes mellitus
 CC type 2, hyperglycaemia, myotonic muscular dystrophy, acanthosis,
 CC nigricans, retinopathy, nephropathy, arteriosclerosis, peripheral
 CC arterial disease) or cancer (e.g. adenocarcinoma, leukaemia, breast
 CC cancer, prostate cancer, colon cancer, ovarian cancer and many others
 CC given in the specification), autoimmune disease, inflammation and
 CC immunodeficiency. The protein is also useful for discovering
 CC or testing compounds which may be either enhancers or inhibitors of PHIP
 CC function. The present sequence is genomic DNA encoding PHIP and NDRP.

XX SQ Sequence 140036 BP; 48500 A; 25843 C; 22499 G; 43194 T; 0 Other;

Query Match 7.6%; Score 19; DB 24; Length 140036;
 Best Local Similarity 100.0%; Pred No. 17;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 AGTTAAAAATCAGAAAAAT 65
 |||||

Db 128998 AGTTAAAAATCAGAAAAAT 128980

RESULT 14

AAC22654

ID AAC22654 standard; cDNA; 251 BP.

XX AAC22654;

DT 06-OCT-2000 (first entry)

DE Human secreted protein 5' EST, SEQ ID NO: 26729.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.

XX Homo sapiens.

XX EP1033401-A2.

XX 06-SEP-2000.

PF 21-FEB-2000; 2000EP-0200610.

XX 26-FEB-1999; 99US-0122487.

PA (GEST) GENSET.

PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX Claim 1; SEQ ID 26729; 71pp + CD-ROM; English.

PS The present sequence is one of a large number of 5' ESTs derived from

CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from

CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)

CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.
XX
SQ Sequence 251 BP; 92 A; 38 C; 52 G; 69 T; 0 other;

Query Match 7.2%; Score 18; DB 21; Length 251;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 TTGTATTAGGTGTATAA 154
|||||
Db 81 TTGTATTAGGTGTATAA 98

RESULT 15
ABN16703
ID ABN16703 standard; cDNA; 286 BP.

AC ABN16703;

DT 24-JUN-2002 (first entry)

DE Human ORFX polynucleotide sequence SEQ ID NO:1883.

XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
XX hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis; gene; ss.

XX Homo sapiens.

XX WO200192523-A2.

XX 06-DEC-2001.

XX 29-MAY-2001; 2001WO-US10836.

XX 30-MAY-2000; 2000US-206132P.

XX 29-AUG-2000; 2000US-228716P.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach MD;

XX WPI; 2002-106308/14.

XX P-PSDB; ABP00951.

XX Novel human polypeptides and polynucleotides useful for diagnosing,
XX preventing and treating cardiovascular disease, neurodegenerative,
XX hyperproliferative disorders and autoimmune disorders -

XX Disclosure; SEQ ID 1883; 1037pp; English.

XX The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification). ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP0010 to ABP11500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated
CC disorder in humans, and in the manufacture of a medicament for treating a
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,

CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative disorders, disorders related to organ
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC storage disease, various immune deficiencies and disorders, infectious
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, or periodontal disease, and for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage.

CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 286 BP; 77 A; 71 C; 58 G; 80 T; 0 other;

Query Match 7.2%; Score 18; DB 24; Length 286;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 TTTTATTACAAAAATA 114

|||||

Db 140 TTTTATTACAAAAATA 157

Search completed: February 13, 2003, 04:59:25

Job time : 340 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.
OM nucleic - nucleic search, using sw model
Run on: February 13, 2003, 04:52:47 ; Search time 67 Seconds
(without alignments)
1139.739 Million cell updates/sec
Title: US-09-895-435-4
Perfect score: 249
Sequence: 1 ggggtaccgcagcatttcg.....gacgcggaggaaatcacatg 249
Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0
Searched: 441362 seqs, 153338381 residues
Word size : 0

Total number of hits satisfying chosen parameters: 882724
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 45 summaries
Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	17	6.8	439	US-09-397-787-269	Sequence 269, App
C 2	17	6.8	1029	US-09-330-611-3	Sequence 3, Appli
C 3	17	6.8	12124	US-08-181-271A-36	Sequence 36, Appl
C 4	17	6.8	12124	US-08-449-315-36	Sequence 36, Appl
C 5	17	6.8	12124	US-08-449-315-36	Sequence 36, Appl
C 6	17	6.8	12124	US-08-449-043-36	Sequence 36, Appl
C 7	17	6.8	12124	US-08-456-265A-36	Sequence 36, Appl
C 8	17	6.8	12124	US-08-455-416-36	Sequence 36, Appl
C 9	17	6.8	12124	US-08-455-244-36	Sequence 36, Appl
C 10	17	6.8	12124	US-08-454-876-36	Sequence 36, Appl
C 11	17	6.8	12124	US-08-457-364-36	Sequence 36, Appl
C 12	17	6.8	12124	US-08-456-262-36	Sequence 36, Appl
C 13	17	6.8	12124	US-08-456-240-36	Sequence 36, Appl
C 14	17	6.8	12124	US-08-455-736-36	Sequence 36, Appl
C 15	17	6.8	12124	US-08-971-217-36	Sequence 36, Appl
C 16	17	6.8	12124	US-09-350-600-36	Sequence 36, Appl
C 17	17	6.8	18596	US-09-318-448-11	Sequence 36, Appl
C 18	17	6.8	50000	US-09-146-053-4	Sequence 11, Appl
C 19	17	6.8	168575	US-09-426-290-1	Sequence 4, Appli
C 20	16	6.4	240	US-09-134-001C-2403	Sequence 2403, Ap
C 21	16	6.4	264	US-09-134-001C-2149	Sequence 2149, Ap
C 22	16	6.4	319	US-07-593-657-14	Sequence 14, Appl
C 23	16	6.4	417	US-09-134-001C-482	Sequence 482, App
C 24	16	6.4	978	US-08-858-207A-174	Sequence 174, App
C 25	16	6.4	999	US-08-961-527-193	Sequence 193, App
C 26	16	6.4	1241	US-07-593-657-6	Sequence 6, Appli
C 27	16	6.4	1241	US-08-942-012B-3	Sequence 3, Appli

28 16 6.4 2061 4 US-09-653-839-7 Sequence 7, Appli
29 16 6.4 2109 4 US-09-653-839-5 Sequence 5, Appli
30 16 6.4 2172 4 US-09-653-839-3 Sequence 3, Appli
31 16 6.4 2220 4 US-09-653-839-1 Sequence 1, Appli
32 16 6.4 2510 4 US-08-894-324A-2 Sequence 2, Appli
33 16 6.4 2806 4 US-09-653-839-9 Sequence 9, Appli
34 16 6.4 3839 4 US-09-245-248B-57 Sequence 57, Appli
35 16 6.4 3854 2 US-08-720-484A-1 Sequence 1, Appli
36 16 6.4 3854 3 US-08-953-823A-1 Sequence 1, Appli
37 16 6.4 3854 4 US-09-398-239-1 Sequence 1, Appli
38 16 6.4 4337 3 US-09-187-049-1 Sequence 1, Appli
39 16 6.4 5181 1 US-08-257-073-10 Sequence 10, Appli
40 16 6.4 13965 4 US-09-453-702B-48 Sequence 48, Appli
41 16 6.4 15225 2 US-08-892-403A-2 Sequence 2, Appli
42 16 6.4 99500 4 US-09-798-096-10 Sequence 10, Appli
43 15 6.0 339 4 US-09-134-001C-1040 Sequence 1040, Ap
44 15 6.0 432 4 US-09-071-035-129 Sequence 129, App
45 15 6.0 453 4 US-09-134-001C-2262 Sequence 2262, Ap

ALIGNMENTS

RESULT 1
US-09-397-787-269/c
; Sequence 269, Application US/09397787
; Patent No. 6468758
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN
; FILE REFERENCE: 210121.466C2
; CURRENT APPLICATION NUMBER: US/09/397,787
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 269
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Homo sapien
; NAME/KEY: misc_feature
; LOCATION: (1)...(439)
; OTHER INFORMATION: n = A,T,C or G
US-09-397-787-269

Query Match 6.8%; Score 17; DB 4; Length 439;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 ATTCCTTGACACATACA 90
Db 142 ATTCCTTGACACATACA 126
|||||

RESULT 2
US-09-330-611-3
; Sequence 3, Application US/09330611
; Patent No. 6248874
; GENERAL INFORMATION:
; APPLICANT: FREY, Perry A.
; APPLICANT: RUZICKA, Frank J.
; TITLE OF INVENTION: DNA MOLECULES ENCODING BACTERIAL LYSINE 2,3-AMINOMUTASE
; FILE REFERENCE: 032026/0476
; CURRENT APPLICATION NUMBER: US/09/330,611
; CURRENT FILING DATE: 1999-06-11
; EARLIER APPLICATION NUMBER: US 09/198,942
; EARLIER FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0

```
; SEQ ID NO 3
; LENGTH: 1029
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1026)
US-09-330-611-3

Query Match
Best Local Similarity 100.0%; DB 4; Length 1029;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 TATAGACGGGAGGAAA 242
|||||
DB 102 TATAGACGGGAGGAAA 118

RESULT 3
US-08-181-271A-36/c
; Sequence 36, Application US/08181271A
; Patent No. 5614395
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/181,271A
; FILING DATE: 13-JAN-94
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667

; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Cucumis sativus
; INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
; IMMEDIATE SOURCE:
; CLONE: pBscuccchrt5
US-08-181-271A-36

Query Match
Best Local Similarity 100.0%; DB 1; Length 12124;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AAAAAATCAGAAATAT 67
|||||
DB 11018 AAAAAATCAGAAATAT 11002

RESULT 4
US-08-449-315-36/c
; Sequence 36, Application US/08449315
; Patent No. 5650505
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
```

```

; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,315
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129

```

```

; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Cucumis sativus
; INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
; IMMEDIATE SOURCE:
; CLONE: pBsgucchrcht5
; US-08-449-315-36

Query Match 6.8%; Score 17; DB 1; Length 12124;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AAAAAATCAGAAAATAT 67
|||||
Db 11018 AAAAAATCAGAAAATAT 11002

RESULT 5
US-08-444-803-36/c
; Sequence 36, Application US/08444803
; Patent No. 5654414
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,803
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993

```

RESULT 6
US-08-449-043-36/c
; Sequence 36, Application US/08449043
; Patent No. 5689044


```
;
;
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 35,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Cucumis sativus
; INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
; IMMEDIATE SOURCE:
; CLONE: pBScucchrcht5
;
; US-08-449-043-36
;
; Query Match 6.8%; Score 17; DB 1; Length 12124;
; Best Local Similarity 100.0%; Pred. No. 16;
; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 51 AAAAAATCAGAAATAT 67
   |||||||
Db 11018 AAAAAATCAGAAATAT 11002

RESULT 7
US-08-456-265A-36/c
; Sequence 36, Application US/08456265A
; Patent No. 5767369
; GENERAL INFORMATION:
; APPLICANT: Alexander, Danny C.
; APPLICANT: Ryals, John A.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Stinson, Jeffrey R.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,265A
; FILING DATE: 31-MAY-95
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/181,271
; FILING DATE: 13-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
```

```
;
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Cucumis sativus
; INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
; IMMEDIATE SOURCE:
; CLONE: pBScucchrcht5
;
; US-08-456-265A-36
;
; Query Match 6.8%; Score 17; DB 1; Length 12124;
; Best Local Similarity 100.0%; Pred. No. 16;
; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 51 AAAAAATCAGAAATAT 67
   |||||||
Db 11018 AAAAAATCAGAAATAT 11002

RESULT 8
US-08-455-416-36/c
; Sequence 36, Application US/08455416
; Patent No. 577200
; GENERAL INFORMATION:
```

Thu Feb 13 12:35:00 2003

APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,416
FILING DATE: 31-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672

FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 12124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORGANISM: Cucumis sativus
INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
IMMEDIATE SOURCE:
CLONE: pBScucchrcht5
US-08-455-416-36
Query Match 6.8% Score 17: DB 1; Length 12124:
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 51 AAAAAATCAGAAATAT 67
|||||
Db 11018 AAAAAATCAGAAATAT 11002
RESULT 9
US-08-455-244-36/c
Sequence 36, Application US/08455244
Patent No. 5789214
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,244
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 12124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Cucumis sativus
INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
IMMEDIATE SOURCE:
CLONE: pBScuecchrcht5
US-08-455-244-36

Query Match 6.8% Score 17; DB 1; Length 12124;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AAAAAATCAGAAATAT 67
|||||
Db 11018 AAAAAATCAGAAATAT 11002
RESULT 10
US-08-454-876-36/c
Sequence 36, Application US/08454876
Patent No. 5804693
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,876
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989

Thu Feb 13 12:35:00 2003

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Cucumis sativus
; INDIVIDUAL ISOLATE: Cucurbit Chitinase Genomic DNA
; IMMEDIATE SOURCE:
; CLONE: pBSCucchrht5
;
; US-08-454-876-36
;
; Query Match 6.8%; Score 17; DB 1; Length 12124;
; Best Local Similarity 100.0%; Pred. No. 16;
; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 51 AAAAAATCAGAAATAT 67
; |||||
; DB 11018 AAAAAATCAGAAATAT 11002
;
; RESULT 11
; US-08-457-364-36/C
; Sequence 36, Application US/08457364
; Patent No. 5847258
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,364
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,157
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

```
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Cucumis sativus
; INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
; IMMEDIATE SOURCE:
; CLONE: pBScucchrht5
US-08-457-364-36
```

```
Query Match 6.8%; Score 17; DB 2; Length 12124;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 51 AAAAAATCAGAAATAT 67
      |||||||
Db 11018 AAAAAATCAGAAATAT 11002
```

```
RESULT 12
US-08-456-262-36/C
; Sequence 36, Application US/08456262
; Patent No. 5851766
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,262
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Cucumis sativus
; INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
; IMMEDIATE SOURCE:
; CLONE: pBScucchrht5
US-08-456-262-36
```

```
Query Match 6.8%; Score 17; DB 2; Length 12124;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AAAAAATCAGAAATAT 67
      |||||||
Db 11018 AAAAAATCAGAAATAT 11002
```

```
RESULT 13
US-08-456-240-36/C
; Sequence 36, Application US/08456240
; Patent No. 5856154
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
```

```

; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Cucumis sativus
; INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
; IMMEDIATE SOURCE:
; CLONE: pBScuccchrt5
; US-08-456-240-36

Query Match          6.8%; Score 17; DB 2; Length 12124;
Best Local Similarity 100.0%; Pred.No.16;
Matches 17; Conservative 0; Mismatches 0; Indels 0;

QY      51 AAAAAATCAGAAATAT 67
        |||||
DB      11018 AAAAAATCAGAAATAT 11002

RESULT 14
US-08-455-736-36/c
; Sequence 36, Application US/08455736
; Patent No. 5880328
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Heins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,736
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-1994
; APPLICATION NUMBER: US 08/093,301

```

; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT 1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/PL/COC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Cucumis sativus
; INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
; IMMEDIATE SOURCE:
; CLONE: pBSucchrht5
; US-08-455-736-36

Query Match 6.8% Score 17; DB 2; Length 12124;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AAAAATCAGAAATAT 67
 |||||
Db 11018 AAAAATCAGAAATAT 11002

RESULT 15
US-08-971-217-36/c
; Sequence 36, Application US/08971217

; Patent No. 5942662
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Harms, Christian
; APPLICANT: Friedrich, Leslie
; APPLICANT: Beck, James
; APPLICANT: Utnes, Scott
; APPLICANT: Ward, Eric
; TITLE OF INVENTION: INDUCIBLE HERBICIDE RESISTANCE
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NO. 5942662artis Corporation
; STREET: 3054 Cornwallis Road, P.O. Box 12257
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,217
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/457,364
; FILING DATE: 31-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/181,271
; FILING DATE: 13-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT 1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/PL/COC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Cucumis sativus
; INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
; IMMEDIATE SOURCE:
; CLONE: pBSucchrht5
; US-08-455-736-36

Thu Feb 13 12:35:00 2003

FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV5/CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 12124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Cucumis sativus
INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
IMMEDIATE SOURCE:
CLONE: pBScucchrcht5
US-08-971-217-36

Query Match 6.8%; Score 17; DB 2; Length 12124;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AAAAAATCAGAAATAT 67
|||||
Db 11018 AAAAAATCAGAAATAT 11002

Search completed: February 13, 2003, 06:42:21
Job time : 89 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 13, 2003, 04:56:57 : Search time 114 Seconds
(without alignments)
1112.470 Million cell updates/sec

Title: US-09-895-435-4
Perfect score: 249
Sequence: 1 ggggtaccgcagcatttcg.....gacgcggaggaaatcacatg 249

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 424239 seqs, 254661826 residues

Word size : 0

Total number of hits satisfying chosen parameters: 848478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications, NA.*

```
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	38	15.3	5230	10	US-09-838-718A-5
C 2	38	15.3	5770	10	US-09-838-718A-7
C 3	38	15.3	5870	10	US-09-838-718A-8
C 4	38	15.3	5906	10	US-09-838-718A-6
C 5	19	7.6	1566	10	US-09-070-927A-535
C 6	18	7.2	341	10	US-09-960-352-2720
C 7	18	7.2	457	10	US-09-864-761-3543
C 8	18	7.2	1500	9	US-09-938-842A-4541
C 9	18	7.2	2000	9	US-09-938-842A-4002
C 10	18	7.2	4704	10	US-09-818-512-3
C 11	18	7.2	116592	10	US-09-818-512-3
C 12	18	7.2	640681	10	US-09-790-988-1
C 13	17	6.8	148	10	US-09-962-436-517
C 14	17	6.8	309	10	US-09-969-373-1246
C 15	17	6.8	433	10	US-09-974-300-5415
C 16	17	6.8	439	10	US-09-876-889-269
C 17	17	6.8	1029	9	US-09-847-010-3
C 18	17	6.8	2000	9	US-09-938-842A-2876
C 19	17	6.8	2000	9	US-09-938-842A-3160

C 20	17	6.8	2389	9	US-10-098-841-192
C 21	17	6.8	2531	10	US-09-070-927A-96
C 22	17	6.8	4610	9	US-09-984-001-1
C 23	17	6.8	4735	10	US-09-967-552A-71
C 24	17	6.8	5676	10	US-09-764-877-3756
C 25	17	6.8	6019	10	US-09-764-847-1719
C 26	17	6.8	6479	9	US-10-098-841-101
C 27	17	6.8	11057	9	US-09-764-868-1308
C 28	17	6.8	18596	9	US-09-954-531-124
C 29	17	6.8	18596	9	US-09-954-531-348
C 30	17	6.8	18596	10	US-09-880-107-1590
C 31	17	6.8	18596	10	US-09-967-768A-119
C 32	17	6.8	41104	10	US-09-816-685-3
C 33	17	6.8	99916	10	US-09-816-095-3
C 34	17	6.8	180557	12	US-10-003-806-6
C 35	17	6.8	180557	12	US-10-003-806-9
C 36	17	6.8	197957	10	US-09-822-246-3
C 37	16	6.4	22	9	US-10-113-877-174
C 38	16	6.4	222	10	US-09-974-300-4140
C 39	16	6.4	250	10	US-09-783-590-16
C 40	16	6.4	257	10	US-09-964-824A-69
C 41	16	6.4	301	10	US-09-960-352-13603
C 42	16	6.4	328	10	US-09-967-768A-302
C 43	16	6.4	368	10	US-09-867-701-3705
C 44	16	6.4	381	9	US-09-796-692-7000
C 45	16	6.4	391	10	US-09-983-965-503

ALIGNMENTS

RESULT 1

US-09-838-718A-5/c

; Sequence 5, Application US/09838718A

; Patent No. US20020019043A1

; GENERAL INFORMATION:

; APPLICANT: Steidler, Lothar

; APPLICANT: Remaut, Erik R.

; APPLICANT: Fiers, Walter R.

; TITLE OF INVENTION: USE OF A CYTOKINE-PRODUCING LACTOCOCCUS STRAIN TO TREAT COLITIS

; FILE REFERENCE: 2676-4779US

; CURRENT APPLICATION NUMBER: US/09/838,718A

; PRIOR FILING DATE: 2001-04-19

; PRIOR APPLICATION NUMBER: PCT/EP99/07800

; PRIOR FILING DATE: 1999-10-06

; PRIOR APPLICATION NUMBER: EP 98203529.7

; PRIOR FILING DATE: 1998-10-20

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 5230

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: plasmid pTREX1

US-09-838-718A-5

Query Match 15.3% Score 38; DB 10; Length 5230;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTACCGCCAGCATTTCGGAAAAAACACCGCTAAG 38
|||||
Db 2323 GGGGTACCGCCAGCATTTCGGAAAAAACACCGCTAAG 2286

RESULT 2

US-09-838-718A-7/c

; Sequence 7, Application US/09838718A

; Patent No. US20020019043A1

; GENERAL INFORMATION:

; APPLICANT: Steidler, Lothar

; APPLICANT: Remaut, Erik R.

Thu Feb 13 12:35:01 2003

us-09-895-435-4.rnpb

```
; APPLICANT: Fiers, Walter R.
; TITLE OF INVENTION: USE OF A CYTOKINE-PRODUCING LACTOCOCCUS STRAIN TO TREAT COLITIS
; FILE REFERENCE: 2676-4779US
; CURRENT APPLICATION NUMBER: US/09/838,718A
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: PCT/EP99/07800
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: EP 98203529.7
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.1
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
; TYPE: DNA
; LENGTH: 5770
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pTLM1L10
US-09-838-718A-7

Query Match      15.3%; Score 38; DB 10; Length 5770;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTACCGCCAGCATTTCCGAAAAAAACACCGCTAAG 38
   |||||||||||||||||||||||||||||||||||||||
Db 2863 GGGTACCGCCAGCATTTCCGAAAAAAACACCGCTAAG 2826

RESULT 3
US-09-838-718A-8/c
; Sequence 8, Application US/09838718A
; Patent No. US20020019043A1
; GENERAL INFORMATION:
; APPLICANT: Steidler, Lothar
; APPLICANT: Remaut, Erik R.
; APPLICANT: Fiers, Walter R.
; TITLE OF INVENTION: USE OF A CYTOKINE-PRODUCING LACTOCOCCUS STRAIN TO TREAT COLITIS
; FILE REFERENCE: 2676-4779US
; CURRENT APPLICATION NUMBER: US/09/838,718A
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: PCT/EP99/07800
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: EP 98203529.7
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; TYPE: DNA
; LENGTH: 5870
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pTITR5AH
US-09-838-718A-8

Query Match      15.3%; Score 38; DB 10; Length 5870;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTACCGCCAGCATTTCCGAAAAAAACACCGCTAAG 38
   |||||||||||||||||||||||||||||||||||||||
Db 2963 GGGTACCGCCAGCATTTCCGAAAAAAACACCGCTAAG 2926

RESULT 4
US-09-838-718A-6/c
; Sequence 6, Application US/09838718A
; Patent No. US20020019043A1
; GENERAL INFORMATION:
; APPLICANT: Steidler, Lothar
; APPLICANT: Remaut, Erik R.
; APPLICANT: Fiers, Walter R.
; TITLE OF INVENTION: USE OF A CYTOKINE-PRODUCING LACTOCOCCUS STRAIN TO TREAT COLITIS
; FILE REFERENCE: 2676-4779US
US-09-838-718A-6

Query Match      15.3%; Score 38; DB 10; Length 5906;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTACCGCCAGCATTTCCGAAAAAAACACCGCTAAG 38
   |||||||||||||||||||||||||||||||||||||||
Db 2999 GGGTACCGCCAGCATTTCCGAAAAAAACACCGCTAAG 2962

RESULT 5
US-09-070-927A-535
; Sequence 535, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunsch
; APPLICANT: Patrick J. Dillon
; APPLICANT: Steven Barash
; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 982
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,927A
; FILING DATE: 04-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,655
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: 60/044,031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: 60/066,009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 535:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1566 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 535:
US-09-070-927A-535
```

```

Query Match          7.6%  Score 19;  DB 10;  Length 1566;
Best Local Similarity 100.0%;  Pred. No. 4;
Matches 19;  Conservative 0;  Mismatches 0;  Gaps 0;

QY  98 TTTTATACAAAAATAAT 116
    |||||||
DB  1489 TTTTATACAAAAATAAT 1507

RESULT 6
US-09-960-352-2720/c
; Sequence 2720, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 2720
; LENGTH: 341
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 12-LIB34-013-Q1-EL-C7
US-09-960-352-2720

Query Match          7.2%  Score 18;  DB 10;  Length 341;
Best Local Similarity 100.0%;  Pred. No. 12;
Matches 18;  Conservative 0;  Mismatches 0;  Gaps 0;

QY  209 TTAGACGCAACAATTT 226
    |||||||
DB  253 TTAGACGCAACAATTT 236

RESULT 7
US-09-864-761-3543
; Sequence 3543, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmics-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30

```

```

; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 3543
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007966.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.61
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.71
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.88
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.91
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.99
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
US-09-864-761-3543

Query Match          7.2%  Score 18;  DB 10;  Length 457;
Best Local Similarity 100.0%;  Pred. No. 12;
Matches 18;  Conservative 0;  Mismatches 0;  Gaps 0;

QY  137 TTGTATTAGGTGTATAA 154
    |||||||
DB  15 TTGTATTAGGTGTATAA 32

RESULT 8
US-09-938-842A-4541
; Sequence 4541, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 4541
; LENGTH: 1500
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4541

```

```
Query Match          7.2%; Score 18; DB 9; Length 1500;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 TACAAAAAATAATACAAC 121
      |||||
Db 419 TACAAAAAATAATACAAC 436

RESULT 9
US-09-938-842A-4002
; Sequence 4002, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPL300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 4002
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4002

Query Match          7.2%; Score 18; DB 9; Length 2000;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 TTTTATACAAAAAATA 114
      |||||
Db 1664 TTTTATACAAAAAATA 1681

RESULT 10
US-09-764-877-3292
; Sequence 3292, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3292
; LENGTH: 4704
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3292

Query Match          7.2%; Score 18; DB 10; Length 4704;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 ATTCCTTCACACATACAT 91
      |||||
Db 1961 ATTCCTTCACACATACAT 1978
```

```
RESULT 11
US-09-818-512-3
; Sequence 3, Application US/09818512
; Patent No. US20020142416A1
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al.
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001192
; CURRENT APPLICATION NUMBER: US/09/818,512
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 116592
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(116592)
; OTHER INFORMATION: n = A,T,C or G
US-09-818-512-3

Query Match          7.2%; Score 18; DB 10; Length 116592;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 137 TTGTATTAGGTGTTTATA 154
      |||||
Db 94442 TTGTATTAGGTGTTTATA 94459

RESULT 12
US-09-790-988-1/c
; Sequence 1, Application US/09790988
; Patent No. US20020127687A1
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEMI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match          7.2%; Score 18; DB 10; Length 640681;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 TTTTATACAAAAAATA 114
      |||||
Db 483308 TTTTATACAAAAAATA 483291

RESULT 13
US-09-962-436-517/c
; Sequence 517, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
```

;
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-75
; CURRENT APPLICATION NUMBER: US/09/962,436
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,082
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/234,924
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 517
; LENGTH: 148
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-436-517

Query Match 6.8%; Score 17; DB 10; Length 148;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 AAAATAATACACACAA 125
|||||
Db 138 AAAATAATACACACAA 122

RESULT 14
US-09-969-373-1246/c
; Sequence 1246, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US/09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US/09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 1246
; LENGTH: 309
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-1246

Query Match 6.8%; Score 17; DB 10; Length 309;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 TTATATAATAATAAT 165
|||||
Db 267 TTATATAATAATAAT 251

RESULT 15
US-09-974-300-5415/c
; Sequence 5415, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526

;
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5415
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Bacillus clausii
US-09-974-300-5415

Query Match 6.8%; Score 17; DB 10; Length 433;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 ACATGTTCTTTTAT 104
|||||
Db 32 ACATGTTCTTTTAT 16

Search completed: February 13, 2003, 07:01:29
Job time : 298 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 13, 2003, 03:18:01 : Search time 2282 Seconds
(without alignments)
1767.167 Million cell updates/sec

Title: US-09-895-435-4
Perfect score: 249
Sequence: 1 999gtaccgcagcattcg.....gacgcgaggagaatcacatg 249

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

```

1: em_estba:*
2: em_esthum:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estio:*
8: em_htc:*
9: gb_esti:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_tod:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	8.8	796	17	AQ782108 HS_3174_B
2	21	8.4	534	17	CNS00NSF
3	21	8.4	561	17	BH781624
4	21	8.4	584	17	AQ967791
5	21	8.4	588	17	AZ527276
6	21	8.4	607	17	AG138789

7	8.4	726	17	BH860734
21	8.4	1180	17	B10174
20	8.0	191	10	AW481697
20	8.0	277	12	BG631395
11	8.0	331	13	B1187613
12	8.0	353	13	B1345004
13	8.0	411	13	B1191005
14	8.0	420	17	AQ058794
15	8.0	462	10	AV682443
16	8.0	718	17	AG174222
17	8.0	818	17	A2538703
18	8.0	920	12	BF275297
19	7.6	263	13	B1744903
20	7.6	382	12	BF396290
21	7.6	386	13	BM406353
22	7.6	399	17	A2741082
23	7.6	401	17	AQ953948
24	7.6	429	14	BM958869
25	7.6	441	9	AU229838
26	7.6	442	17	AQ600207
27	7.6	443	12	BG603695
28	7.6	450	17	AZ175162
29	7.6	453	17	AZ175164
30	7.6	457	17	BH213219
31	7.6	458	13	BM111491
32	7.6	460	17	AZ285657
33	7.6	474	13	BM113619
34	7.6	474	13	BM407225
35	7.6	474	13	BM407275
36	7.6	474	13	BM407323
37	7.6	474	13	BM407330
38	7.6	474	13	BM407331
39	7.6	474	13	BM407401
40	7.6	474	13	BM407411
41	7.6	474	13	BM407418
42	7.6	474	13	BM407443
43	7.6	478	13	BM111174
44	7.6	491	17	CNS06078
45	7.6	507	13	BM109770

ALIGNMENTS

RESULT 1
AQ782108
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

AQ782108
HS_3174_B1_D08_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3174 Col=15 Row=H, DNA sequence.
AQ782108
AQ782108.1 GI:5685068
GSS.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 796)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu

[illegible]

For additional information, see <http://www.tigr.org/tdb/at/at.html>
 Seq primer: TR
 Class: shotgun.

FEATURES
 source
 1..584
 Location/Qualifiers

/organism="Arabidopsis thaliana"
 /strain="Landsberg erecta"
 /db_xref="taxon:3702"
 /clone="LERIV03"
 /clone_lib="LERG"
 /note="Organ: Leaf; Vector: pUC19K; Total genomic DNA was sheared to 0.4-0.7 kbp before ligation."

BASE COUNT 199 a 99 c 118 g 168 t

Query Match 8.4%; Score 21; DB 17; Length 584;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 TTAATAATCAGAAATATAT 69
 |||||
 Db 78 TTAATAATCAGAAATATAT 98

RESULT 5
 A527276/c
 LOCUS 588 bp DNA linear GSS 07-MAY-2001
 DEFINITION 266pbE11 Pb MBN #21 Plasmodium berghei genomic 3', DNA sequence.
 ACCESSION A527276
 VERSION A527276.1 GI:13969913
 KEYWORDS GSS.

ORGANISM Plasmodium berghei.
 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 1 (bases 1 to 588)
 AUTHORS Carlton, J.M.-R. and Dame, J.B.

TITLE The Plasmodium vivax and P. berghei gene sequence tag projects
 JOURNAL Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)
 COMMENT Contact: Dame JB
 Dept. of Pathobiology, College of Veterinary Medicine
 University of Florida
 2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA
 Tel: 352 392 4700
 Fax: 352 392 9704
 Email: damej@mail.vetmed.ufl.edu

Seq primer: M13(-20) forward
 Class: shotgun.

FEATURES
 source
 1..588
 Location/Qualifiers

/organism="Plasmodium berghei"
 /strain="ANKA clone 15cyl (clone of the ANKA 8417 clone)"
 /db_xref="taxon:5821"
 /clone_lib="Pb MBN #21"
 /dev_stage="asexual blood forms"
 /lab_host="Mus musculus"
 /note="Vector: pBluescript SK(+) vector DNA, phagemid excised from lambda ZAP; Site_1: EcorV; Site_2: EcorV;
 Genomic DNA was prepared from asynchronous blood stage forms of the cloned ANKA isolate of P. berghei grown in laboratory Swiss white mice. The DNA was purified from contaminating host DNA by Hoechst Dye 33258-CSCI ultracentrifugation and precipitated. Purified DNA was digested with mung bean nuclease in the presence of 36-38% formamide at 50 C, as described (Vernick, K.D., Imberski, R.B., and McCutchan, T.F. 1988. Nucleic Acids Research 16:6883-6896). The ends of the digestion fragments were polished using T4 DNA polymerase, and the fragments size selected in the range 500-2000 bp. These were ligated into the EcorV-cleaved and dephosphorylated pBluescript SK(+) vector. Recombinant plasmids were used to transform E. coli XL10-Gold host cells."

BASE COUNT 218 a 74 c 87 g 209 t

Query Match 8.4%; Score 21; DB 17; Length 588;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 AAAATAATACAAACAATATT 129
 |||||
 Db 311 AAAATAATACAAACAATATT 291

RESULT 6
 AG138789/c
 LOCUS 607 bp DNA linear GSS 04-NOV-2001
 DEFINITION Pan troglodytes DNA, clone: PTB-153B07.F, genomic survey sequence.
 ACCESSION AG138789
 VERSION AG138789.1 GI:16668467
 KEYWORDS GSS.
 SOURCE Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male

ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 1
 AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

TITLE BAC end sequences of Library PTB
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 607)
 AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

TITLE Direct Submission
 JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimpbes@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
 COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS
 Sequencing: -21M13
 LIBRARY Vector : pKS145
 R.Site 1 : SacI
 R.Site 2 : SacI.
 Location/Qualifiers

1..607
 /organism="Pan troglodytes"
 /db_xref="taxon:9598"
 /clone="PTB-153B07.F"
 /sex="male"
 /cell_type="lymphoblast"
 /clone_lib="PTB Chimpanzee Male BAC Library"

BASE COUNT 216 a 41 c 142 g 187 t
 ORIGIN

Query Match 8.4%; Score 21; DB 17; Length 607;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 TTTTATTATACAAAATAAT 116
 |||||
 Db 333 TTTTATTATACAAAATAAT 313

RESULT 7
 BH860734
 LOCUS 726 bp DNA linear GSS 08-JUL-2002
 DEFINITION ORNL233 Poplar BAC Library Populus balsamifera subsp. trichocarpa genomic, DNA sequence.

ACCESSION BH860734
 VERSION BH860734.1 GI:21711555
 KEYWORDS GSS.

TITLE
 Sequence evaluation of four pooled-tissue normalized bovine cDNA
 libraries and construction of a gene index for cattle
JOURNAL
 Genome Res. 11 (4), 626-630 (2001)
MEDLINE
 21180013
COMMENT
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@mail.marc.usda.gov
 Single pass sequencing. Bases called and trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 20
 and -minmatch 12 options.
 PCR Primers
 FORWARD: AGGAACACGCTATGACCAT
 BACKWARD: GTTTCACGTCACGACG
 Plate: 22 row: D column: 4
 Seq primer: ATTACGTCACACTATAG.
 Location/Qualifiers

FEATURES source

1..191
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="MARC IBOV"
 /tissue_type="pooled"
 /lab_host="DH108"
 /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
 Library made from pooled tissue from lymph node, ovary,
 fat, hypothalamus, and pituitary."
 56 a 42 c 30 g 63 t

BASE COUNT
ORIGIN
 Query Match 8.0%; Score 20; DB 10; Length 191;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 TTTTATACAAAAATAA 115
 |||||
Db 182 TTTTATACAAAAATAA 163

RESULT 10
LOCUS
DEFINITION
 BG631395 277 bp mRNA linear EST 19-APR-2001
 cC-esf1cLEL7K03a1 Tomato flower library from a mixture of
 developmental stages Lycopersicon esculentum cDNA clone
 cc-esf1cLEL7K03a1, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
 Lycopersicon.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
 1 (bases 1 to 277)
 van der Hoeven,R.S. and Tanksley,S.D.
 ESTs from a tomato flower library
 Unpublished (2001)
 Contact: Rutgers S. van der Hoeven
 Cornell University
 252 Emerson Hall, Ithaca, NY 14850, USA
 Tel: 607 255 7886
 Fax: 607 255 6683
 Email: rv19@cornell.edu
 3 prime sequence.

FEATURES
 Location/Qualifiers
 1..277
 /organism="Lycopersicon esculentum"
 /cultivar="E6203"
 /db_xref="taxon:4081"
 /clone="cc-esf1cLEL7K03a1"

/clone_lib="Tomato flower library from a mixture of
 developmental stages"
 /tissue_type="developing flower buds and open flowers"
 /dev_stage="4-8 week old plants"
 /lab_host="XL0LR"
 /note="Vector: pBK CMV; Site_1: EcoRI; Site_2: XhoI;
 Flowers and flower buds were collected from greenhouse
 grown plants and used for library construction (cLEL)."
 92 a 47 c 34 g 104 t

BASE COUNT
ORIGIN
 Query Match 8.0%; Score 20; DB 12; Length 277;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 TTTATACAAAAATATACA 119
 |||||
Db 39 TTTATACAAAAATATACA 58

RESULT 11
LOCUS
DEFINITION
 BI187613 331 bp mRNA linear EST 10-JUL-2001
 bib01fs.f1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
 library Fusarium sporotrichioides cDNA clone bib01fs 3', mRNA
 sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 BI187613
 BI187613.1 GI:14661292
 EST.
 Fusarium sporotrichioides.
 Fusarium sporotrichioides.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE
AUTHORS
 Ren,Q., Tag,A., Pielow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
 ,M. and Roe,B.
 Analysis of a Fusarium sporotrichioides EST database
 Unpublished (2001)
 Other_ESTs: bib01fs.r1

TITLE
JOURNAL
COMMENT
 Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu

Contact Dr. Marian Beremand regarding clone availability Included
 is the best homolog from a blastx search of Genbank nr 04-09-01
 68 5.5 gi|1376187|ref|NP_0 hypothetical protein FLJ23554
 [Homosapiens
 Seq primer: M13-20
 High quality sequence stop: 318.

FEATURES
 Location/Qualifiers
 1..331
 /organism="Fusarium sporotrichioides"
 /strain="Tri 10"
 /db_xref="taxon:5514"
 /clone="bib01fs"
 /clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
 cDNA library"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
 XhoI; 3' end of cDNA cloned into XhoI site of pBluescript"
 92 a 77 c 69 g 93 t

BASE COUNT
ORIGIN
 Query Match 8.0%; Score 20; DB 13; Length 331;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 AGAGTTAAAAATCAGAAAA 64
 |||||
Db 309 AGAGTTAAAAATCAGAAAA 328

```

RESULT 12
BI345004
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 353)
AUTHORS
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCGCCAGTCACGACG
Plate: 121 row: I column: 6
Seq primer: ATTTAGGTGACACTATAG.
FEATURES
Location/Qualifiers
1..353
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT
80 a 80 c 98 g 95 t
ORIGIN
1
TTCCTTTTATACAAAAA 112
|||||
259 TTCCTTTTATACAAAAA 278

Query Match 8.0%; Score 20; DB 13; Length 353;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 TTCCTTTTATACAAAAA 112
|||||
Db 259 TTCCTTTTATACAAAAA 278

RESULT 13
BI191005
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Fusarium sporotrichioides.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.
REFERENCE
1 (bases 1 to 411)
AUTHORS
Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
,M. and Roe,B.
* TITLE
Analysis of a Fusarium sporotrichioides EST database

Unpublished (2001)
Other_ESTs: j2f05fs.r1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
71 3.6 gll13376187/ref|NP_0 hypothetical protein FLJ23554
[Homosapiens]
Seq primer: M13-20
High quality sequence stop: 313.
FEATURES
Location/Qualifiers
1..411
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone_lib="j2f05fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
; 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT
115 a 99 c 85 g 112 t
ORIGIN
1
AGAGTTAAAAAATCAGAAA 64
|||||
301 AGAGTTAAAAAATCAGAAA 320

Query Match 8.0%; Score 20; DB 13; Length 411;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 AGAGTTAAAAAATCAGAAA 64
|||||
Db 301 AGAGTTAAAAAATCAGAAA 320

RESULT 14
AQ058794/c
LOCUS
DEFINITION
PCII11-52A23.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-52A23,
DNA sequence.
ACCESSION
AQ058794
VERSION
AQ058794.1 GI:3348755
KEYWORDS
GSS.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 420)
AUTHORS
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
Venter,J.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
Unpublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Class: BAC ends.
FEATURES
Location/Qualifiers
1..420
/organism="Homo sapiens"

```

Job time : 2292 secs

/db_xref="GDB:7519606"
 /db_xref="taxon:9606"
 /clone="RPCI-11-52A23"
 /clone_lib="RPCI-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
 RPCI11 Human Male BAC Library"

BASE COUNT 122 a 84 c 63 g 151 t
 ORIGIN

Query Match 8.0%; Score 20; DB 17; Length 420;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 GTGTTATATAATAATAAT 165
 |||||
 DB 340 GTGTTATATAATAATAAT 321

RESULT 15

AV682443 462 bp mRNA linear EST 16-JAN-2002
 LOCUS AV682443 GKB Homo sapiens cDNA clone GKBAD11 5', mRNA sequence:
 ACCESSION AV682443
 VERSION AV682443.1 GI:10284306
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
 Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
 Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
 Hu, G., Gu, J., Chen, Z., and Han, Z.

TITLE Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
 21625106

JOURNAL

MEDLINE
 COMMENT Contact: Zequang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919(ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

FEATURES

source Location/Qualifiers
 1..462
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="GKBAD11"
 /clone_lib="GKB"
 /tissue_type="hepatocellular carcinoma"
 /dev_stage="Adult"
 /lab_host="SOLR"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
 XhoI"

BASE COUNT 186 a 70 c 58 g 148 t
 ORIGIN

Query Match 8.0%; Score 20; DB 10; Length 462;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 TTTATACAAAATAATACA 119
 |||||
 Db 368 TTTATACAAAATAATACA 387

Search completed: February 13, 2003, 06:30:44

THIS PAGE BLANK (USPTO)